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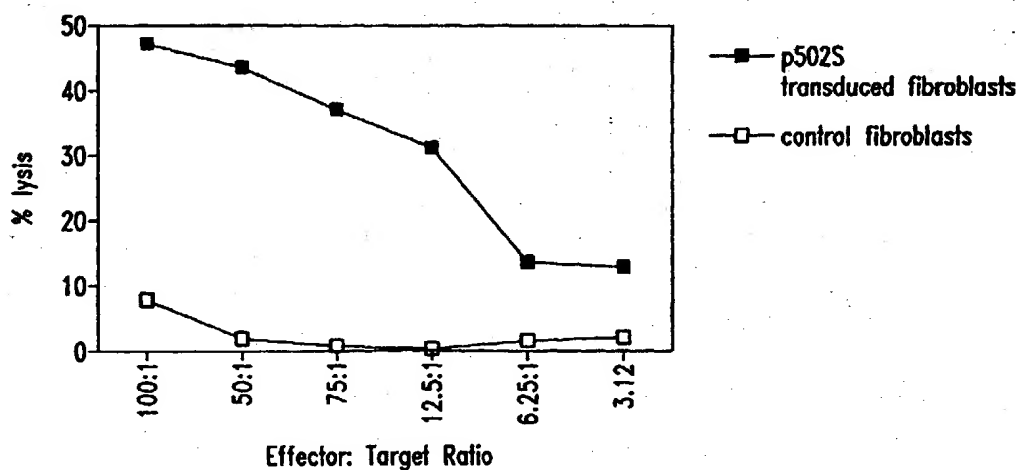
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(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.

WO 01/25272 A2

COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating

such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount

detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17

SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17

SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12

SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12

SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862

SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862

SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13

SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13

SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19

SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19

SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25

SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25

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SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)
SEQ ID NO: 108 is the predicted amino acid sequence for F1-12
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SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2

SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6

SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10
SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
SEQ ID NO: 307 is the determined cDNA sequence for P711P
SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
SEQ ID NO: 312 is the determined cDNA sequence for P715P
SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5

SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26

SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26

SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23

SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23

SEQ ID NO: 332 is the determined full length cDNA sequence for P509S

SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)

SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.
SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
SEQ ID NO: 384 is the cDNA sequence for P1000C.
SEQ ID NO: 385 is the cDNA sequence for CGI-82.
SEQ ID NO:386 is the cDNA sequence for 23320.
SEQ ID NO:387 is the cDNA sequence for CGI-69.
SEQ ID NO:388 is the cDNA sequence for L-iditol-2-dehydrogenase.
SEQ ID NO:389 is the cDNA sequence for 23379.
SEQ ID NO:390 is the cDNA sequence for 23381.
SEQ ID NO:391 is the cDNA sequence for KIAA0122.
SEQ ID NO:392 is the cDNA sequence for 23399.
SEQ ID NO:393 is the cDNA sequence for a previously identified gene.
SEQ ID NO:394 is the cDNA sequence for HCLBP.
SEQ ID NO:395 is the cDNA sequence for transglutaminase.
SEQ ID NO:396 is the cDNA sequence for a previously identified gene.
SEQ ID NO:397 is the cDNA sequence for PAP.
SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.
SEQ ID NO:399 is the cDNA sequence for hTGR.
SEQ ID NO:400 is the cDNA sequence for KIAA0295.
SEQ ID NO:401 is the cDNA sequence for 22545.
SEQ ID NO:402 is the cDNA sequence for 22547.
SEQ ID NO:403 is the cDNA sequence for 22548.
SEQ ID NO:404 is the cDNA sequence for 22550.
SEQ ID NO:405 is the cDNA sequence for 22551.
SEQ ID NO:406 is the cDNA sequence for 22552.
SEQ ID NO:407 is the cDNA sequence for 22553.
SEQ ID NO:408 is the cDNA sequence for 22558.
SEQ ID NO:409 is the cDNA sequence for 22562.
SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.
SEQ ID NO:412 is the cDNA sequence for 22568.
SEQ ID NO:413 is the cDNA sequence for 22570.
SEQ ID NO:414 is the cDNA sequence for 22571.
SEQ ID NO:415 is the cDNA sequence for 22572.
SEQ ID NO:416 is the cDNA sequence for 22573.
SEQ ID NO:417 is the cDNA sequence for 22573.
SEQ ID NO:418 is the cDNA sequence for 22575.
SEQ ID NO:419 is the cDNA sequence for 22580.
SEQ ID NO:420 is the cDNA sequence for 22581.
SEQ ID NO:421 is the cDNA sequence for 22582.
SEQ ID NO:422 is the cDNA sequence for 22583.
SEQ ID NO:423 is the cDNA sequence for 22584.
SEQ ID NO:424 is the cDNA sequence for 22585.
SEQ ID NO:425 is the cDNA sequence for 22586.
SEQ ID NO:426 is the cDNA sequence for 22587.
SEQ ID NO:427 is the cDNA sequence for 22588.
SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.

SEQ ID NO:441 is the cDNA sequence for 22853.
SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.
SEQ ID NO:451 is the cDNA sequence for 23614.
SEQ ID NO:452 is the cDNA sequence for 23618.
SEQ ID NO:453 is the cDNA sequence for 23622.
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
SEQ ID NO:455 is the cDNA sequence for LIM protein.
SEQ ID NO:456 is the cDNA sequence for a known gene.
SEQ ID NO:457 is the cDNA sequence for a known gene.
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
SEQ ID NO:459 is the cDNA sequence for 23045.
SEQ ID NO:460 is the cDNA sequence for 23032.
SEQ ID NO:461 is the cDNA sequence for 23054.
SEQ ID NOs:462-467 are cDNA sequences for known genes.
SEQ ID NOs:468-471 are cDNA sequences for P710P.
SEQ ID NO:472 is a cDNA sequence for P1001C.
SEQ ID NO:473 is the amino acid sequence for PSMA.
SEQ ID NO:474 is the amino acid sequence for PAP.
SEQ ID NO:475 is the amino acid sequence for PSA.
SEQ ID NO:476 is the amino acid sequence for a fusion protein containing PSA, P703P and P501S.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions,

usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are

capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may

also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., In Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera

and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most

preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression

vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be

targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

In certain embodiments, the present invention provides fusion proteins comprising a polypeptide disclosed herein together with at least one of the following known prostate antigens: prostate specific antigen (PSA); prostatic acid phosphatase (PAP); and prostate specific membrane antigen (PSMA). The protein sequences for PSMA, PAP and PSA are provided in SEQ ID NO: 473-475, respectively. In certain embodiments, the fusion proteins of the present invention comprise PSA, PAP and/or PSMA in combination with one or more of the following the inventive antigens: P501S (amino acid sequence provided in SEQ ID NO: 113); P703P (amino acid sequences provided in SEQ ID NO: 327, 329, 331); P704P (cDNA sequence provided in SEQ ID NO: 67); P712P (cDNA sequence provided in SEQ ID NO: 308); P775P (cDNA sequence provided in SEQ ID NO: 311); P776P (cDNA sequence provided in SEQ ID NO: 354); P790P (cDNA sequence provided in SEQ ID NO: 352). The amino acid sequence of a fusion protein of PSA, P703P and P501S is provided in SEQ ID NO: 476. In preferred embodiments, the inventive fusion proteins comprise one of the following combinations of antigens: PSA and P703P; PSA and P501S; PAP and P703P; PAP and P501S; PSMA and P703P; PSMA and P501S; PSA, PAP and P703P; PSA, PAP and P501S; PSA, PAP, PSMA and P703P, PSA, PAP, PSMA and P501S. One of skill in the art will appreciate that the order of polypeptides within a fusion protein can be altered without substantially changing the therapeutic, prophylactic or diagnostic properties of the fusion protein.

The fusion proteins described above are more immunogenic and will be effective in a greater number of prostate cancer patients than any of the individual components alone. The use of multiple antigens in the form of a fusion protein also lessens the likelihood of immunologic escape.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide

components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-

terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal

indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested

by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively,

detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions

or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner

et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be

formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt.

MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific

immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into

dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be

pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g., intracutaneous,*

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from

the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%,

preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter

performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise

at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones

having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E.*

coli DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 μ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the

driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193,

respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA⁺ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-

expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive

cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to

previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor

compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor

and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both microarray technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively.

The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted

amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were

separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, Sall and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig

valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be

expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8); as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells

as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 μ g/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald *et al.* (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μ g of P1S #10 and 120 μ g

of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed ($2\mu\text{g/ml}$ P1S#10 and 10mg/ml $\beta 2$ -microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of $7\mu\text{g/ml}$ dextran sulfate and $25\mu\text{g/ml}$ LPS for 3 days). Six days later cells ($5 \times 10^5/\text{ml}$) were restimulated with $2.5 \times 10^6/\text{ml}$ peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and $3 \times 10^6/\text{ml}$ A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10⁴ fibroblasts in the presence of 3 μ g/ml human β_2 -microglobulin and 1 μ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 8

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

EXAMPLE 9

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured

overnight by the addition of 3 μ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100 μ g of p5 peptide together with 140 μ g of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro*

stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

EXAMPLE 12

ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8⁺ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (⁵¹Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above and Lalvani et al., J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 13

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I
Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as

compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-idoitol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of

normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped

(aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the

expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III

Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were

identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV

Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P

433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57
439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more

substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of

SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.

27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-

binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.

42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.

46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.

47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.

52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

(i) a polypeptide according to claim 1;

(ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or

- (iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;

- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

- (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:
- (i) a polypeptide according to claim 1;
 - (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
 - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
 - (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);
- such that T cells proliferate;
- (b) cloning at least one proliferated cell; and
 - (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
 - (i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and
 - (ii) complements of the foregoing polynucleotides;
- (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is prostate cancer.

62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

63. A method according to claim 62, wherein the binding agent is an antibody.

64. A method according to claim 63, wherein the antibody is a monoclonal antibody.

65. A method according to claim 62, wherein the cancer is a prostate cancer.

66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor

protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 21; and
- (b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

79. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 77; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

1/6

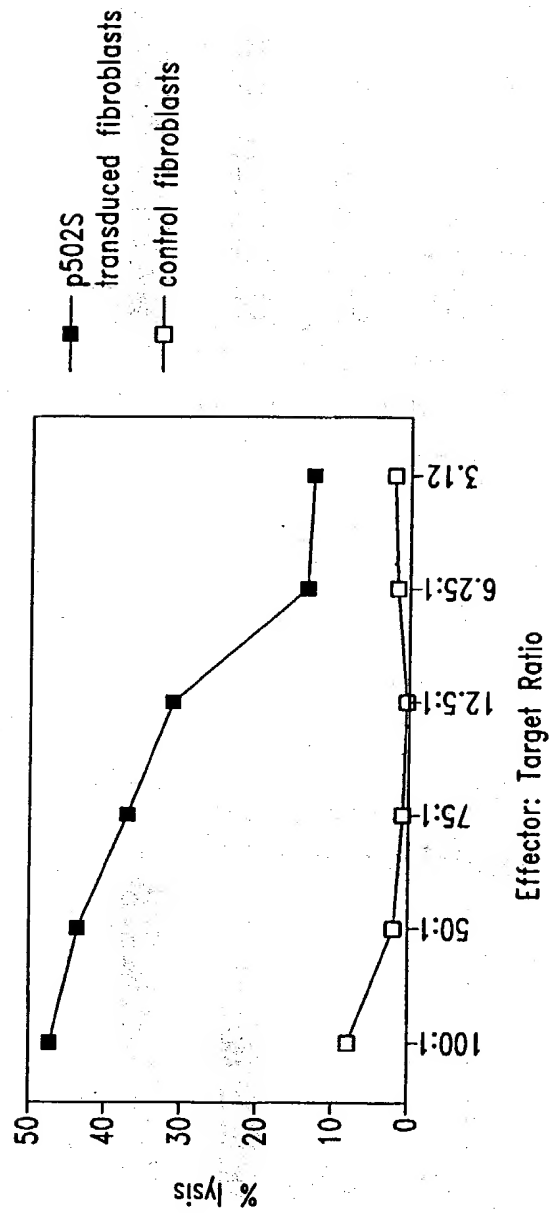
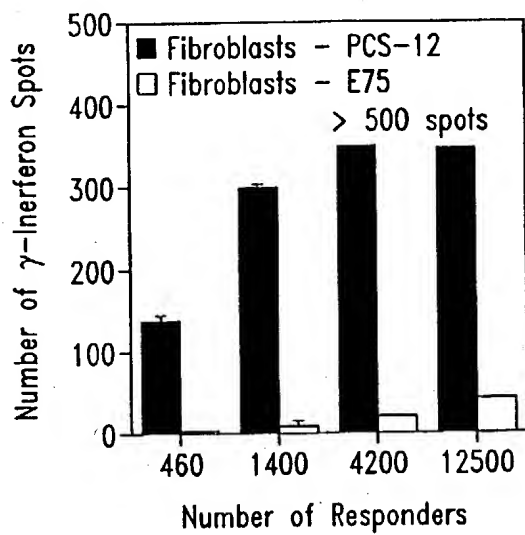
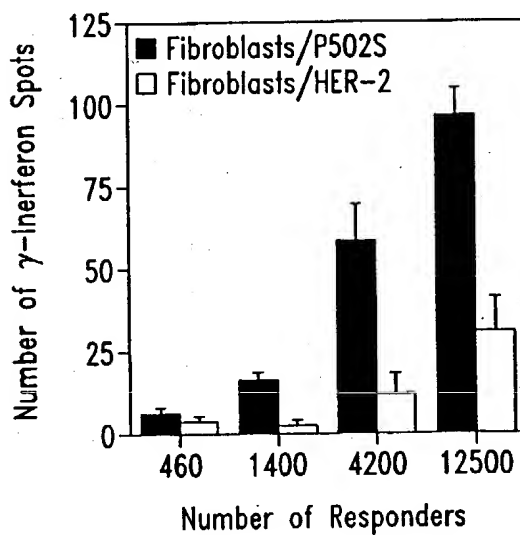


Fig. 1

2/6

*Fig. 2A**Fig. 2B*

3/6

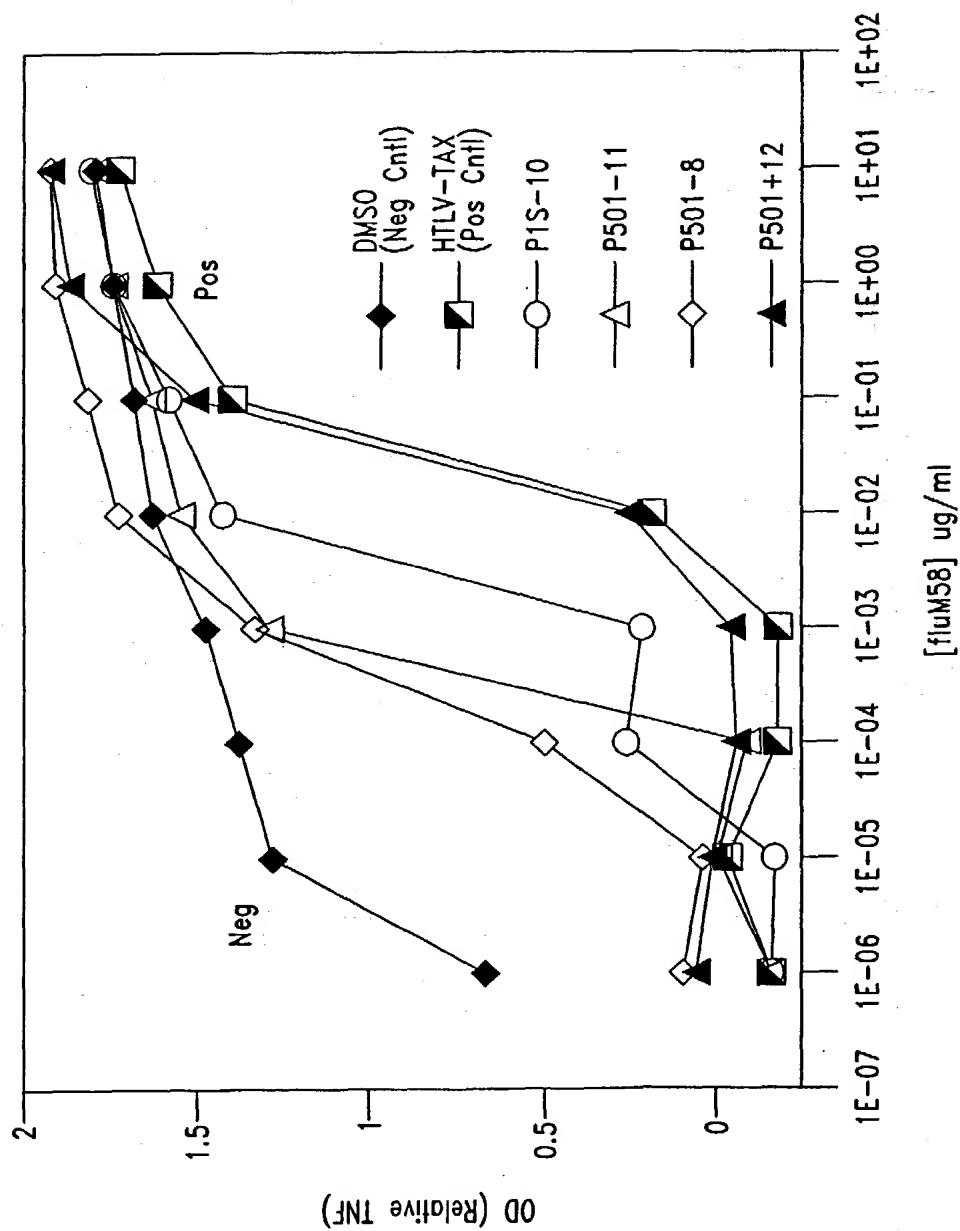


Fig. 3

4/6

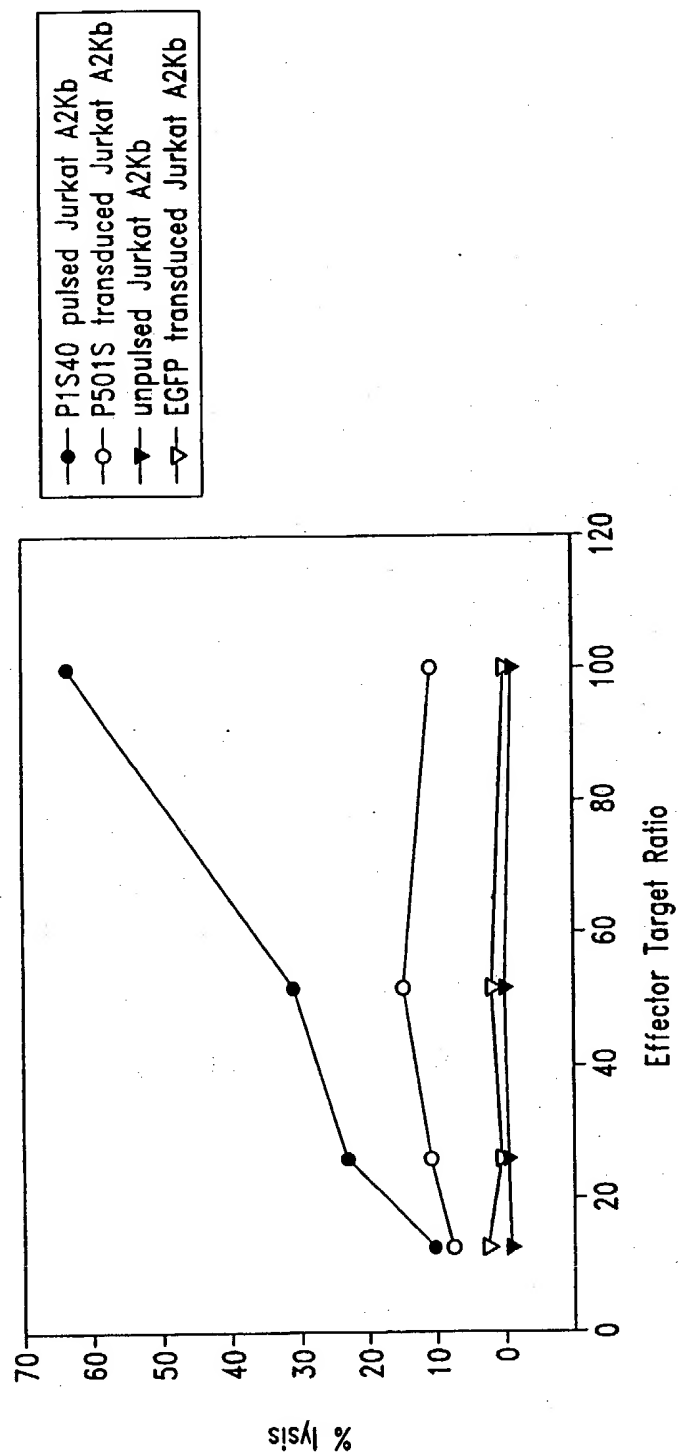


Fig. 4

5/6

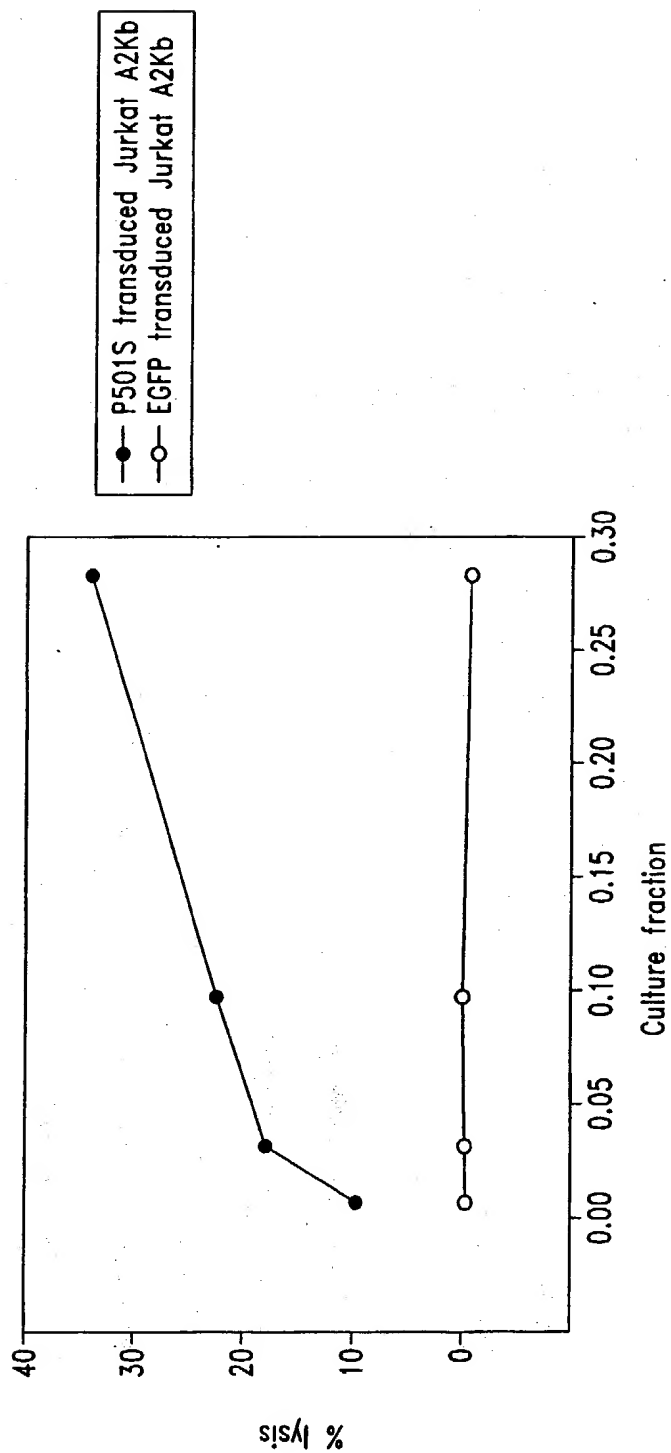
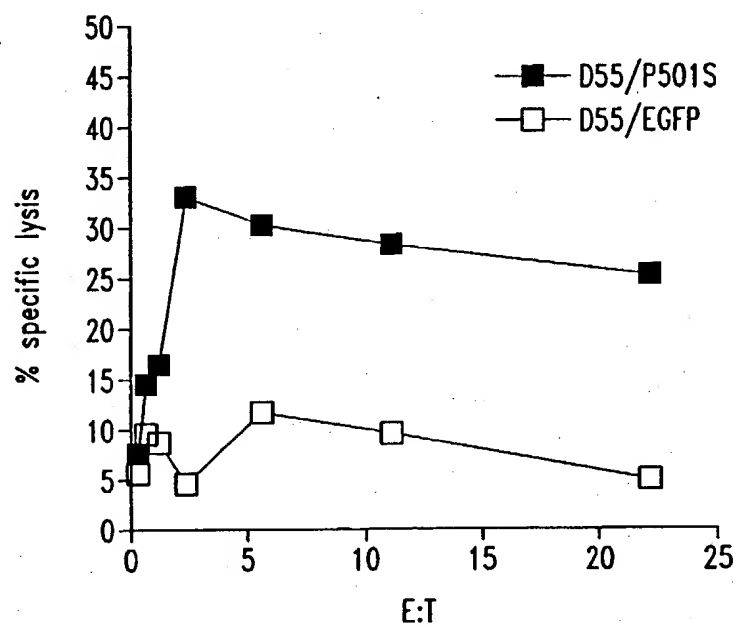
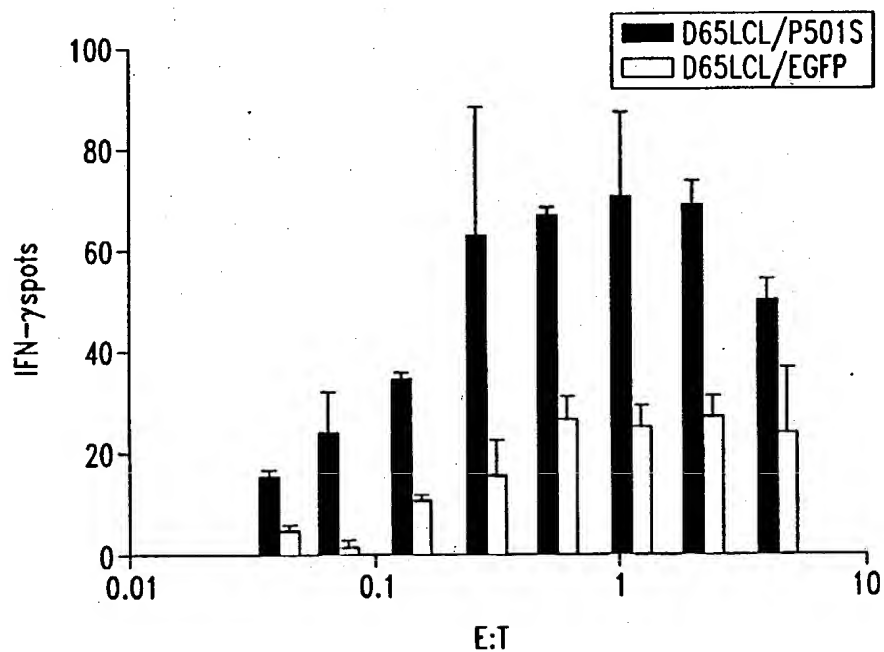


Fig. 5

6/6

*Fig. 6A**Fig. 6B*

SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

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 <223> n = A,T,C or G

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cttttgaaag	aagggatggc	tgggggtgtt	aacagcagag	gtgcagggcg	gggggtcacg	60
tctgtctcct	cactggtgat	aaacgagccc	cgttccttgt	tgtgatcatg	atgaacaacc	120
tctcaaaaag	tcagaaccgg	agtcacacag	gcattctgtc	cgtaaaagat	ttgacaccac	180
tctgccttcg	tcttctttgc	aaatacatct	gcaaacttct	tcttcatttc	tgccaatca	240
tccatgctca	tctgattggg	aagttcatca	gacttttagtc	canntccttt	gatcagcagc	300
tcgtagaact	ggggttctat	tgctccaaca	gccatgaatt	ccccatctgc	tgctcgttaa	360
gtcgtataga	aagggtgctc	accatccaac	atgttctgtc	ctcgaggggg	ggcccgggtac	420
ccaattcgcc	ctatantgag	tcgtattacg	cgcgctcact	ggccgctcgt	ttacaacgtc	480
gtgactggga	aaacctggg	cgttaccaac	ttaatcgctt	tgacgacat	ccccctttcg	540
ccagctgggc	gtaatancca	aaaggcccg	accgatcgcc	cttccaacag	ttgcgcacct	600
gaatgggnaa	atgggacccc	cctgttaccg	cgcattnaac	ccccgcnggg	tttngttgtt	660
acccccacnt	nnaccgctta	cactttgcc	gcgccttanc	gcccgtctcc	tttnccttt	720
cttcccttcc	tttncnccn	ctttccccg	gggtttcccc	ontcaaacc	cna	773

<210> 4
 <211> 828
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(828)
 <223> n = A,T,C or G

<400> 4						
cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggctgc	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatgtt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgttggt	tgtgggggtc	agagatggga	gggggtgggg	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaagga	tgacnctgta	aacatagccc	acgtgtcct	360
gngggcactg	ggaagcctan	atnaggccgt	gagcanaaag	aaggggagga	tccactagtt	420
ctanagcggc	cgcacccg	gtgganctcc	ancctttgtt	cccttttagt	aggggttaatt	480
gcgcgcttgg	cntaatcatg	gtcatanctn	tttctctgtg	gaaattgtta	tccgctcaca	540
attccacaca	acatacganc	cggaaacata	aantgtaaac	ctgggggtgcc	taatgantga	600
ctaactcaca	ttaattgcgt	tgcgctcact	gcccgttttc	caatcnggaa	acctgtcttg	660
ccncttgcat	tnatgaaten	gccaaacccc	ggggaaaagc	gtttgcgttt	tgggcgctct	720
tccgcttctc	cnctcantta	ntccctncnc	tcggtcattc	cggctgcngc	aaaccgggtc	780
accnctcca	aaggggggtat	tccggtttcc	ccnaatccgg	gganancc		828

<210> 5
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(834)
 <223> n = A,T,C or G

<400> 5

tttttttttt	tttttactga	tagatggaat	ttattaagct	tttcacatgt	gatagcacat	60
agttttaatt	gcatccaaag	tactaacaaa	aactctagca	atcaagaatg	gcagcatgtt	120
attttataac	aatcaacacc	tgtggctttt	aaaatttggg	tttcataaga	taattttatc	180
tgaagtaaat	ctagccatgc	ttttaaaaaa	tgcttttagg	caactccaagc	ttggcagtta	240
acatttggtc	taaaacaata	taaaacaatc	acaatttaac	aaataacaaa	tacaacattg	300
tagggcataa	tcatatacag	tataaggaaa	aggtggtagt	gttgagtaag	cagttattag	360
aatagaatac	cttggcctct	atgcaaatat	gtctagacac	tttgattcac	tcagccctga	420
cattcagttt	tcaaagtagg	agacaggttc	tacagtatca	ttttacagtt	tccaacacat	480
tgaaaacaag	tagaaaatga	tgagttgatt	tttattaatg	cattacatcc	tcaagagtta	540
tcaccaaccc	ctcagttata	aaaaattttc	aagttatatt	agtcataata	cttggtgtgc	600
ttattttaaa	ttagtgtctaa	atggattaag	tgaagacaac	aatgggtccc	taatgtgatt	660
gatattggtc	atttttacca	gcttctaaat	ctnaactttc	aggcttttga	actggaacat	720
tgatnatac	tggtccanag	ttncaccta	ctggaacatt	acagtgtgct	tgattcaaaa	780
tggtattttg	ttaaaaatta	aattttaacc	tggtggaaaa	ataatttgaa	atna	834

<210> 6
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 6

tttttttttt	tttttttttt	aagaccctca	tcaatagatg	gagacatata	gaaatagtca	60
aaccacatct	acaaaatgcc	agtatcaggc	ggcggcttcg	aagccaaagt	gatgtttgga	120
tgtaaagtga	aatattagtt	ggcggatgaa	gcagatagtg	aggaaagtgt	agccaataat	180
gacgtgaagt	ccgtggaagc	ctgtggctac	aaaaaatggt	gagccgtaga	tgccgtcgga	240
aatgggtgaag	ggagactcga	agtactctga	ggcttgtagg	agggtaaaat	agagaccag	300
taaaattgta	ataagcagtg	cttgaattat	ttggtttcgg	ttgttttcta	ttagactatg	360
gtgagctcag	gtgattgata	ctcctgatgc	gagtaatacg	gatgtgttta	ggagtgggac	420
ttctagggga	tttagcgggg	tgatgcctgt	tgggggccag	tgccctccta	gttggggggt	480
aggggctagg	ctggagtggg	aaaaggctca	gaaaaatcct	gcgaagaaaa	aaacttctga	540
ggtaataaat	aggattatcc	cgtatcgaag	gccttttttg	acaggtgggt	tggtgtggcc	600
ttggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatggtta	gtgtgttggt	660
ttantangg	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggccctgtta	ngggctctgg	ctnggtttta	cccnacccat	780
ggaatncncc	ccccggacna	ntgnatccct	attcttaa			818

<210> 7
 <211> 817
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(817)
 <223> n = A,T,C or G

<400> 7

tttttttttt	tttttttttt	tggtcttaga	gggggttagag	ggggtgctat	agggtaaata	60
cgggccctat	ttcaaagatt	tttaggggaa	tttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggtga	180

aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcgga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctcctag	gttcaatacc	420
attggtggcc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tgttatgtaa	480
aggatnccct	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaata	aanaattaan	tttngttatt	600
gaatnttng	gaaaagggt	tacaggacta	gaaaccaaata	angaaaanta	atnntaangg	660
cnttatcntn	aaaggnata	accnctccta	tnatcccacc	caatngnatt	ccccacnenn	720
acnattggat	nccccanttc	canaaaanggc	cnccccccg	tgnannccnc	cttttgttcc	780
cttnantgan	ggttattenc	ccctngcntt	atcance			817

<210> 8
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 8						
catttccggg	tttactttct	aaggaaagcc	gagcggaagc	tgctaacgtg	ggaatcggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgtcctgggg	240
tgggtggccg	angcctganc	cgtctgcct	tgtgcceccc	angtgggccc	ccacccccctg	300
acctgcctgg	gtccaaacac	tgagccctgc	tggcggactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcggcc	ccccacactg	gttggccttg	420
tctttgangt	gagccccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacia	ccacannatg	cccggctcct	cccggaaacc	antcccancc	tgngaaggat	540
caagncctgn	atccactnnt	nctanaaccg	gcncncnccg	cngtggaaac	cnccttntgt	600
tccttttont	tnagggttaa	tnnccgcttg	gccttncan	ngtcctnccn	nttttccnnt	660
gttnaaattg	ttangcnccc	nccnntcccn	cnnnnncnan	cccgaccenn	annttnnann	720
ncctgggggt	nccnnengat	tgaccenncc	nccctntant	tgenttnggg	nncnntgccc	780
ctttccctct	nggganncg					799

<210> 9
 <211> 801
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 9						
acgccttgat	cctcccaggc	tgggactggt	tctgggagga	gccgggcatg	ctgtgggttg	60
taangatgac	actcccaaag	gtggtcctga	cagtggccca	gatggacatg	gggctcacct	120
caagggacaag	gccaccaggt	gcgggggccc	aagccacat	gacccctact	ctatgagcaa	180
aatccctctg	gggggcttct	ccttgaagtc	cgccancagg	gctcagtctt	tggacccang	240
caggtcatgg	ggttgtnngc	caactggggg	ccncaacgca	aaanggcna	gggcctcngn	300
cacccatccc	angacgcggc	tacactnctg	gacctccncc	tccaccactt	tcatgcgctg	360
ttentacccg	cgnatntgtc	ccanctgttt	cngtgcenac	tccancttct	nggacgtgcg	420
ctacatacgc	ccggantonc	netcccgttt	tgtccctatc	cacgtntccn	caacaaattt	480
cncntantg	cacnatttcc	caenttttnc	agntttccnc	nncngncttc	cttntaaaag	540
ggttganccc	cggaaaatnc	cccaaagggg	gggggcccng	tacccaactn	ccccctnata	600
gctgaantcc	ccatnaccnn	gnctnatgg	ancntccnt	tttaannacn	ttctnaactt	660
gggaananc	ctcgnccntn	ccccnttaa	tccncccttg	cnangnnent	cccccnntcc	720
ncccnntng	gcntntnann	cnaaaaaggc	ccnnnancaa	tctcctnncn	cctcanttcg	780

ccanccctcg aaatcgccn c

801

<210> 10
 <211> 789
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 10
 cagtcctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgccctgtccc 60
 acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc 120
 agatcctgcc ctacacactg gectccctct accaccggga gaagcaggtg ttcttgccca 180
 aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc 240
 caggccctaa gectggagct cccttcctta atggacacgt ggggtgctga ggcagtggcc 300
 tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg 360
 tgggtgggtga gcccaccgan gccagggtgg ttccggggccg gggcatctgc ctggacctgc 420
 ccactctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggtccat 480
 tgtccagctc agccagctctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt 540
 cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg 600
 ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc 660
 tcctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaaantnat 720
 gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780
 gnggttccc 789

<210> 11
 <211> 772
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc feature
 <222> (1)...(772)
 <223> n = A,T,C or G

<400> 11
 cccaccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac 60
 tttgttaaat aaataagtta aatatttaaa tgccctgtgtc tctgtgatgg caacagaagg 120
 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180
 tgtgggctga ggggacctgg ttctgtgtg ttgcccctca ggactcttcc cctacaaata 240
 actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag 300
 ctacattaaa cgaagctgca ggttaagggg cttanagatg gaaaccagg tgactgagtt 360
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480
 ctccctgtat aagtcagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540
 aactggggaa aaaagaaaag gacgccccan ccccagctg tgcanctacg cacctcaaca 600
 gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca 660
 accccggcac cccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca 720
 ggccnccac ccnaatntt gctgggaaat ttttccctcc ctaaatntt tc 772

<210> 12
 <211> 751
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 12
 gccccaattc cagctgccac accaccacag gtgactgcat tagttcggat gtcatacaaa 60
 agctgattga agcaaccctc tacttttttg tctgtgagcct tttgcttggg gcagggtttca 120
 ttggctgtgt tgggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
 aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
 atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300
 ggcactacca gcaacgtcag ggaagtgtct agccattgtg gtgtacacca aggcgaccac 360
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420
 acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna 480
 cnccggctgc gatgaagaaa tnaccccnag ttgacaaact tgcatggcac tggganccac 540
 agtgggccna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600
 ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660
 tnatnaacnt gaaccctgcn tngtggctcc tgttcaggnc cnnngcctga cttctnaann 720
 aangaactcn gaagncccca cngganannc g 751

<210> 13
 <211> 729
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(729)
 <223> n = A,T,C or G

<400> 13
 gagccaggcg tccctctgcc tgcccactca gtggcaacac ccgggagctg ttttgcctt 60
 tgtggancct cagcagtncc ctctttcaga actcantgcc aaganccctg aacaggagcc 120
 accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt 180
 ctgtgtggtg cagccctgtt ggcagtgggc atctgggtgt caatcgatgg ggcacccctt 240
 ctgaagatct tcggggccact gtctgtccagt gccatgcagt ttgtcaacgt gggctacttc 300
 ctcatcgagc ccggcggtgt ggtcttagct ctaggtttcc tgggctgcta tgggtctaag 360
 actgagagca agtgtgccct cgtgacgttc ttcttcatcc tcctcctcat cttcattgct 420
 gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttctgtacgt 480
 tgctggtaat gcctgccatc aaaaaagat tatgggttcc caggaanact tcaactcaagt 540
 gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt 600
 gaagantcac ctacttcaaa gaaaanagtg cctttccccc atttctgttg caattgacaa 660
 acgtcccaa cacagccaat tgaaaacctg caccacaacc aaangggctc ccaaccanaa 720
 attnaaggg 729

<210> 14
 <211> 816
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(816)
 <223> n = A,T,C or G

<400> 14
 tgctcttccct caaagttggt cttgttgcca taacaaccac cataggtaaa gcgggcgcag 60
 tgttcgcgtga aggggttgta gtaccagcgc gggatgctct ccttgacagag tcctgtgtct 120
 ggcaggtcca cgcagtcccc tttgtcactg gggaaatgga tgcgctggag ctctgcaaa 180
 ccactcgtgt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt ggggggtgtct 240
 tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaaactg ggtgggctga 300
 cangtgccag agcacactgg atggcgctt tccatgnnan gggccctgng ggaaagtccc 360
 tganccccan anctgcctct caaangcccc accttgacac ccccgacagg ctagaatgga 420
 atcttcttcc cgaaaggtag ttnttcttgt tgcccaancc anccccntaa acaaactctt 480
 gcanatctgc tccgnggggg tcntantacc ancgtgggaa aagaaccoca ggcngcgaac 540
 caancttgtt tggatncgaa gcnataatct nctnttctgc ttggtggaca gcaccantna 600

ctgtnnanct	ttagnccntg	gtcctcntgg	gttggncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnancntn	ccccctgggt	tgggggttttn	720
cncnctccta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15
 <211> 783
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(783)
 <223> n = A,T,C or G

<400> 15						
ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgcctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtact	gtgctgtcca	240
ccaagcagac	agaagactac	tgcctcgcac	ccaacaangt	gggtcgcgtc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagtg	cattctancc	tgtcnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	cagggcccct	480
ccatggaaaag	gcgccatcca	ntgttctctg	gcacctgtca	gcccacccag	ttccgctgca	540
ncaatggctg	ctgcacnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctccaac	aaagcttccc	tgtnnaaaaa	tacnccantt	ggcttttnac	aaacncccg	660
cncctcctnt	ttccccnntn	aacaaagggc	nctngccttt	gaactgccn	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctgggt	cctnnaance	cctccncaa	anctncccc	780
ccc						816

<210> 16
 <211> 801
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 16						
gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttgg	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagcccttc	240
atggtggtgt	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtag	gaagtgtcga	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgcctc	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcga	atgaaagaaa	ntacccaact	tgacaaactg	catggccact	ggacgacagt	540
tgccccgaan	atcttcagaa	aagggatgcc	ccatcgattg	aacacccana	tgcccactgc	600
cnacagggct	gcncncncn	gaaagaatga	gccattgaag	aaggatcntc	ntggtcttaa	660
tgaactgaaa	ccntgcatgg	tggcccctgt	tcagggtctc	tggcagtga	ttctganaaa	720
aaggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17
 <211> 740
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(740)
 <223> n = A,T,C or G

<400> 17

gtgagagcca	ggcgtccctc	tgccctgccca	ctcagtgcca	acacccggga	gctgttttgt	60
cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgttca	gcttcattaa	gaccatgatg	atcctcttca	atttgcctcat	180
ctttctgtgt	ggtgcagccc	tggtggcagt	gggcatctgg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgccatg	cagtttgtca	acgtgggcta	300
cttctctatc	gcagccggcg	ttgtggctct	tgctcttggt	ttcctgggct	gctatgggtgc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttcttcttc	atcctcctcc	tcctcttcat	420
tgctgaagtt	gcagctgctg	tggtgcgctt	ggtgtacacc	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggctc	caatttctgn	tggtctcccc	aactataccg	600
gaattttgaa	agantcncct	tacttccaaa	aaaaaanant	tgcccttnc	cccnttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720
caaaaaaant	nnaagggtn					740

<210> 18
 <211> 802
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(802)
 <223> n = A,T,C or G

<400> 18

ccgctggttg	cgctgggtcca	gngnagccac	gaagcacgtc	agcatcacaca	gcctcaatca	60
caaggtcttc	cagctgccgc	acattacgca	gggcaagagc	ctccagcaac	actgcatatg	120
ggatacactt	tacttttagca	gccaggggtga	caactgagag	gtgtcgaagc	ttattcttct	180
gagcctctgt	tagtggagga	agattccggg	cttcagctaa	gtagtacagc	tatgtcccat	240
aagcaaacac	tgtgagcagc	cggaaggtag	aggcaaagtc	actctcagcc	agctctctaa	300
cattgggcat	gtccagcagt	tctccaaaca	cgtagacacc	agnggcctcc	agcacctgat	360
ggatgagtgt	ggccagcgct	gcccccttgg	ccgacttggc	taggagcaga	aattgctcct	420
ggttctgccc	tgtcaccttc	acttccgcac	tcatcactgc	actgagtgtg	ggggacttgg	480
gctcaggatg	tccagagacg	tggttccgcc	ccctcnctta	atgacaccgn	ccanncaacc	540
gtcggtctcc	gccgantgng	ttcgctgtnc	ctgggtcagg	gtctgctggc	cncacttgc	600
aancttcgtc	nggcccattg	aattcaccnc	accggaactn	gtangatcca	ctnnttctat	660
aaccggnccg	caccgennnt	ggaactccac	tcttnttnc	tttacttgag	gggttaaggtc	720
acccttnccg	ttaccttggt	ccaaaccntn	cctgtgtcgc	anatngtnaa	tcnggncna	780
tnccanccnc	atangaagcc	ng				802

<210> 19
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 19

cnaagcttcc	aggtnacggg	ccgcnaancc	tgaccnagg	tancanaang	cagnccngcg	60
gagccaccg	tcacgngng	nggtctttat	nggagggggc	ggagccacat	cncgtggacnt	120
cntgacccca	actccccnc	ncncantgca	gtgatgagt	cagaactgaa	ggtnacgtgg	180
caggaaacca	gancaaannc	tgctccnntc	caagtcggcn	nagggggcg	ggctggccac	240
gencatccnt	cnagtgtctn	aaagcccn	cctgtctact	tgtttgagga	acngcnngga	300

catgcccagn	gttanataac	nggcngagag	tnantttgcc	tctcccttcc	ggctgcgcan	360
cgngtntgct	tagnggacat	aacctgacta	cttaactgaa	cccnngaate	tnccnccct	420
ccactaagct	cagaacaaaa	aacttegaca	ccactcantt	gtcacctgnc	tgctcaagta	480
aagtgtaccc	catncccaat	gtntgctnga	ngctctgncc	tgcnttangt	tcggctcctgg	540
gaagacctat	caattnaagc	tatgtttctg	actgcctctt	gtccctgna	acaancnacc	600
cnnnntcca	agggggggnc	ggcccccaat	cccccaacc	ntnaattnan	tttancccn	660
ccccnggcc	cggcctttta	cnancntenn	nnacngggna	aaaccnnngc	tttncccaac	720
nnaatcncnc	t					731

<210> 20
 <211> 754
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(754)
 <223> n = A,T,C or G

<400> 20	
tttttttttt	60
caacccccctc	120
annttaaatt	180
tnancctnaa	240
aaatngttna	300
nnccaattgt	360
ggnnancccc	420
gancccnccg	480
ggttngggnc	540
ccaggtgag	600
ggggcctggg	660
tttgntcnc	720
agtcnnttgn	754

<210> 21
 <211> 755
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(755)
 <223> n = A,T,C or G

<400> 21	
atcancccat	60
nngtnagnnc	120
nncanatncc	180
ccagctgtcc	240
nncnncanat	300
cgaaggcnct	360
aactcancn	420
aaaaanaten	480
ttagnngtcc	540
ctttcngaca	600
gggctentct	660
aaattcntnc	720
aaaaggttgt	755

<210> 22
 <211> 849
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagagget	tactacaant	gtgaanacgt	60
acgctnngan	taangcgacc	cgantttctag	ganncnccct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cggaanggtc	accggnngat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactcng	nggccttgcc	caccaccttc	ggcggcccg	ngnccgggcc	cgggtcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	ncccnncng	accnggcga	tccggggtn	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccgnccc	ctttaccct	nnacaagcca	360
cngccttcta	nccnngccc	cccctccant	nngggggact	gccnanngt	ccgttctng	420
nnaccccnnn	gggtncctcg	gttgctgant	cnaccgnang	ccanggatc	cnaaggaagg	480
tgcgttnttg	gccccaccc	ttcgtcncgg	nncacccttc	ccgacnanga	nccgctccc	540
cnccnccng	cctcncctcg	caacacccgc	netentcngt	ncggnnnccc	ccccaccgc	600
nccctcnc	ngnccnanc	ctcncnccc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggngacnng	nagcncntc	gcncgcgc	gcgnccct	cgccncgaa	720
ctncntcngg	ccantnncgc	tcaanccna	cnaaacgcg	ctgcgcggcc	cgnagcgnc	780
ncctcncga	gtcctcccgn	cttcnacc	angnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaaacta	tacttcgctc	gnactcgtgc	gcctcgtcnc	tcttttctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatchan	aagntcganc	agtccaaact	gantaacaca	120
cacacnncan	aganaaatcc	nctgccttcc	anagtanaacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgca	atntgtcnc	gtttattntn	ccagctcnc	240
ctnccnacc	tactcttccn	nagctgtcnn	accctngtn	cgnaccccc	naggctcgga	300
tccgggtttnn	nntgaccgng	cnnccctcc	ccccntccat	nacganccnc	ccgcaccacc	360
nanngcncgc	nccccgnnet	cttcgcnc	ctgtcctntn	ccccgtngc	ctggcncngn	420
accgcattga	ccctcgccnn	ctnchnngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnnngcg	tctgcncgc	gttccttccn	nccncttcca	ccatcttct	tacngggct	540
ccncgcctc	tcnnncacnc	cctgggacgc	tntcctntgc	cccccttnac	tccccctt	600
cgcgtgncc	cgnccccacc	ntcatttnca	nacgntcttc	acaannncct	ggntnnctcc	660
cnancngncn	gtcanccnag	ggaaggngg	ggnnccnntg	nttgacgttg	nggngangtc	720
cgaanantcc	tcncntcan	cctaccct	cgggcgnnet	ctcngttnc	aacttancaa	780
ntctcccccg	ngngcncntc	tcagcctcnc	ccncccnct	ctctgcantg	tncctctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

gcatgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catgggtenta	60
netgncttcc	tgtgtcaaat	gtatacnaaa	tanatatgaa	tctnatntga	caaganngta	120
tentncatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattncgn	180
cgcattcnch	gcncantatn	taatngggaa	ntcnntnnnn	ncaccnncat	ctatcntncc	240
gcncctgac	tggagagat	ggatnatttc	tnntntgacc	nacatgttca	tcttggattn	300
aananccccc	cgcngnccac	cggttngnng	cnagccnntc	ccaagacctc	ctgtggaggt	360
aacctgcgtc	aganncatca	aacntgggaa	accgcgnccc	angtnnaagt	ngnnncanan	420
gatecccgcc	aggnttnacc	atcccttcnc	agcgccecc	ttngtgccct	anagnngnagc	480
gtgtccnanc	cnetcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccta	gggggantna	tncaaaancc	caggattgtc	cncncangaa	atcccncanc	600
ccnccctac	ccnctttgg	gacngtgacc	aantcccgga	gtncaggtcc	ggccngnctc	660
ccccaccggt	nnccntgggg	gggtgaanct	cngnntcanc	cngnccaggn	ntcgnaagga	720
accggnccn	ggncgaanng	ancnntcnga	agnccnnt	cgtataacc	cccctcncca	780
ncnncngnt	agntccccc	cngggtnccg	aangg			815

<210> 25

<211> 775

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(775)

<223> n = A,T,C or G

<400> 25

ccgagatgtc	tcgctccgtg	gccttagctg	tgctcgcgt	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcacccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcaccc	atccgacatt	gaanttgact	180
tactgaagaa	tgganagaga	attgaaaaag	tggagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctcntg	tactacactg	aattcacccc	caactgaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnncatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcnttttaat	antgatatgc	ntatacaccc	taccctttat	gnccccaatt	480
tgtaggggtt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccg	cncccnngtn	ngaattgttc	cnnaaccacg	gttggctccc	ccaggtcncc	600
tcttacggaa	gggcctgggc	cnctttncaa	ggttggggga	accnaaaatt	tcncttntgc	660
cncccnccca	cnntcttgng	nnncanttt	ggaacccttc	cnattccctt	tggcctcnna	720
nccttnncta	anaaaacttn	aaancgtngc	naaannttt	acttcccccc	ttacc	775

<210> 26

<211> 820

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(820)

<223> n = A,T,C or G

<400> 26

anattantac	agtgtaatct	tttccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgtctt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catccagag	gggtgagtag	180
ccatcangcc	tccggtggga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgagggtg	cacactataa	acgttaacga	ccnagatnan	cacctgcttc	aagtgcaccc	360
ttcctacgtg	acnaccagn	accnnnaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnnagcact	cacctgcccc	cccatggccg	tnccgntccc	tggtcctgnc	aagggagact	480
ccctgttgga	attncgggga	naccaaggga	nccccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttcgg	gccnntcccc	tcttctctta	cacgccecc	nntactcntc	600
tccctctntt	ntcctgncnc	acttttnacc	ccnnnatttc	ccttnattga	tcggannctn	660

ganattccac tnnccgctnc cntcnatcng naanacnaaa nactntctna cccnggggat 720
 gggnnccctcg ntcacccctct ctttttctct accnccnntt ctttgccctct ccttngatca
 780tccaaccntc gntggccntn cccccccnnn tcccttnecc
 820

<210> 27
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 27
 tctgggtgat ggcctcttcc tcctcaggga cctctgactg ctctgggcca aagaatctct 60
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120
 ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggcgc 180
 ctgctgagca cttccgcccc tcacctgcc cagccctgc catgagctct gggctgggtc 240
 tccgcctcca gggttctgct ctccangca ngccancaag tggcgctggg ccacactggc 300
 ttcttctgct cccntccctg gctctganc tctgtcttcc tgtcctgtgc angcnccttg 360
 gatctcagtt tccctcctc anngaactct gttctgann tcttcantta actntgantt 420
 tatnaccnan tggctgtnc tgtcnactt taatgggccc gaccggctaa tccctccctc 480
 nctcccttcc anttcnnna accngcttnc cntctctcc ccntancccg ccngggaanc 540
 ctctttgcc ctnaccang gccnnnaccg cccntnnctn ggggggcnng gttnctncnc 600
 ctgntnccc cncctcncnt tncctcgtec cncnncgc nngcannttc ncngtcccn 660
 tnnctctten ngntcgnaa ngntcncntn tnnnnngn ngtntntn tccctctcnc 720
 cnnntgnang tnnntnnnc ncngnncccc nnnnnnnnn nggnntnnn tctnncnge 780
 cccnncccc ngnattaag cctcncntct ccggccnc 818

<210> 28
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 28
 aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg 60
 tcccaacatg anggtgnngt tctcttttga angaggggtg ngtttttann ccnggtgggt 120
 gattnaacc cattgtatgg agnnaaagg tttnaggat ttttcggctc ttatcagtat 180
 ntanattcct gtnaatcgga aaatnatntt tcnnccggaa aatnttgctc ccatccgnaa 240
 attnctcccg ggtagtgcatt nttngggggg cngccangtt tcccaggctg ctanaatcgt 300
 actaaagntt naagtgggan tncaaatgaa aacctnncac agagnatccn taccgactg 360
 tnnnttncct tcgcccctntg actctgcnn agcccaatac ccnngngnat gtnccccngn 420
 nnnngcgnnc tgaaannnnc tcngggctnn gancatcang gggtttcgca tcaaaagcnn 480
 cgtttncat naaggcactt tngcctcatc caaccnctng cctcnncca tttngccgtc 540
 nggttncct acgctnntng cncctnnntn ganattttnc ccgcctnggg naancctcct 600
 gnaatgggta gggnccttntc ttttnaccnn gnggtntact aatcnnctnc acgctnctt 660
 tctcnacccc ccccttttt caatcccanc ggcnaatggg gtctccccnn cgangggggg 720
 nnnccann c 731

<210> 29
 <211> 822
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(822)
 <223> n = A,T,C or G

<400> 29
 actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60
 cgctcanacc tcacanccct ccnacnangc ctataangaa nannaataga nctgtncnnt 120
 atntntacnc tcatanncct cnnnaccacac tccctcttaa cccntactgt gcctatngcn 180
 tnntantct ntgcgcctn cnanccaccn gtgggcnac cncnngnatt ctcnatctcc 240
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300
 tccatnantt annntaacta ccactgaent ngactttcnc atnancctct aatttgaatc 360
 tactctgact cccacngcct annnattagc ancntcccc nacnatntct caaccaaacc 420
 ntcaacaacc tatctantct ttcnccaacc nttncctccg atccccnnac aacccccctc 480
 ccaaataccc nccacctgac ncctaaccen caccateccg gcaagccnan ggncatttan 540
 ccactggaat cacnatngga naaaaaaaac ccnaactctc tancncnnat ctccctaana 600
 aatnctcctn naatttactn ncantnccat caanccccacn tgaaacnnaa cccctgtttt 660
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccnctnc 720
 ccnaatgaag gncnccaat cnangaaacg nccntgaaaa ancnaaggca anannntccg 780
 canatcctat ccccttantn ggggncctt nccnngggcc cc 822

<210> 30
 <211> 787
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(787)
 <223> n = A,T,C or G

<400> 30
 cggcgcgctg ctctggcaca tgccctctga atggcatcaa aagtgatgga ctgccattg 60
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
 gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagtcctc atctacatna 180
 gctggaagcc ctggagggcc tctctcgcca gcctcccct tctctccacg ctctccangg 240
 acaccagggg ctccaggcag cccattattc ccagnangac atgggtgttc tccacgcgga 300
 cccatggggc ctgnaaggcc agggctcct ttgacacat ctctcccgtc ctgctggca 360
 ggccgtggga tccactantt ctanaacggg cgcacccnccg gtgggagctc cagcttttgt 420
 tccnttaat gaaggttaat tgncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
 gtgaaattgt ttntcccctc ncnattccnc ncnacatacn aaccgggaan cataaagtgt 540
 taaagcctgg gggtnccctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600
 ccgctttccn ttcnngaaaa ctgtctctcc ctgcnttntt gaatcgcca ccccccnggg 660
 aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaen cctnccgct 720
 cggtcgttnc nggtngcggg gaangggnat nnnctccnc naagggggng agnnngntat 780
 ccccaaa 787

<210> 31
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 31
 tttttttttt ttttttggc gatgctactg ttttaattgca ggaggtggg gtgtgtgtac 60
 catgtaccag ggctattaga agcaagaagg aaggaggag ggcagagcgc cctgctgagc 120
 aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180
 cccgcagggt gggggccacc agtcaggggg tgggagcact acanggggtg ggagtgggtg 240
 gtggtggtn cnaatggcct gncacanatc cctacgatte ttgacacctg gatttcacca 300

ggggaccttc	tggtctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttggtaca	420
tatggttccg	gcccacctct	cccntcnaan	aagtaattca	ccccccccc	ccntctnttg	480
cctgggacct	taantaccca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcnccn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncccnctc	cccatagnan	600
ntttttnct	cantctaatgc	ccccccnggc	aacnatccaa	tcccccccn	tgggggcccc	660
agcccanggc	ccccgnetcg	ggnnnccngn	cncgnantcc	ccaggncttc	ccantcngnc	720
ccnnngcncc	cccgcacgca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncac	780
ctcgcccccc	ccnnegng					799

<210> 32
 <211> 789
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 32						
tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tttttccnag	ggcaggttta	ttgacaacct	cncgggacac	aancaggctg	gggacaggac	120
ggcaacaggc	tccggcgggc	gcggcgggcg	ccctacctgc	ggtaccaa	ntgcagcctc	180
cgctcccgc	tgatnttct	ctgcagctgc	aggatgcct	aaaacagggc	ctcgccctn	240
ggtgggcacc	ctgggatttn	aatttccacg	ggcacaatgc	ggtcgcancc	cctcaccacc	300
nattaggaat	agtggnttta	ccnccnccg	ttggcncact	ccccntggaa	accacttntc	360
gcggctcccg	catctggtct	taaaccttgc	aaacnctggg	gccctctttt	tggttantnt	420
ncngccaca	atcatnactc	agactggcnc	gggctggccc	caaaaaancn	ccccaaaacc	480
ggncatgtc	ttnnccgggt	tgctgcnatn	tncatcacct	cccgggcnca	ncaggncaac	540
ccaaaagtgc	ttgnggccc	caaaaaanc	ccggggggnc	ccagtttcaa	caaagtcac	600
ccccttggcc	cccaaatcct	ccccccgntt	nctgggtttg	ggaaccacag	cctctnnctt	660
tggnnggcaa	gntggntccc	ccttcggggc	cccgtggggc	ccnctctaa	ngaaaacncc	720
ntcctnnnca	ccatccccc	nnngnacgnc	tancaangna	tccctttttt	tanaaacggg	780
ccccccncc						789

<210> 33
 <211> 793
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(793)
 <223> n = A,T,C or G

<400> 33						
gacagaacat	ggtggatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tggtggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtattt	gcaaagaaga	cgaaggcaga	gtggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttgttcat	catgatcaca	300
acaangaacg	gggctcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgccctgcac	360
ctctgctggt	aaacacccca	gccatccctt	ctttcaaaa	ggatccacta	cttctagagc	420
ggncgccacc	gcgggtggagc	tccagctttt	gttcccttta	gtgaggggta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggg	ggtngccctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtccggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncctccc	gctttctcgc	tccctgaant	ccttcccccc	ggtctttcgc	cttgccgcn	780
acggtatcna	cct					793

<210> 34
 <211> 756
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc feature
 <222> (1)...(756)
 <223> n = A,T,C or G

<400> 34
 gccgcgaccg gcatgtacga gcaactcaag ggcgagtggg accgtaaaag ccccaatctt 60
 ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg 120
 ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgtag catactggag 180
 atcggggccc aatggagcat cctacgcaan gacatcccct ccttcgagcg ctacatggcc 240
 cagctcaaatt gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac 300
 cagctcttgg gcctcaacct cctcttctcg ctgtcccaga accgggtggc tgantnccac 360
 acgganttgg ancggtgcc tgcccanga catacanacc aatgtctaca tcnaccacca 420
 gtgtccttga gcaatactga tgganggcag ctaccncaa gtnttcttgg ccnagggtaa 480
 catccccgc cgagagctac accttcttca ttgacatcct gctcgacact atcagggatg 540
 aaaatcgcn ggttgctcca gaaaggtcnc aanaanatcc ttttcnctga aggccccgg 600
 atncnctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttncct 660
 ttactgaggg ttnattgccg cccttggcgt tatcatggtc acnccngttn cctgtgttga 720
 aattnttaac cccccacaat tccacgcna catnng 756

<210> 35
 <211> 834
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc feature
 <222> (1)...(834)
 <223> n = A,T,C or G

<400> 35
 ggggatctct anactnacct gnatgcatgg ttgtcgggtg ggtcgctgtc gatgaanatg 60
 aacaggatct tgcccttgaa gctctcggtc gctgtnttta agttgctcag tctgccgtca 120
 tagtcagaca cnctcttggg caaaaaacan caggatntga gtcttgattt cacctccaat 180
 aatcttcngg gctgtctgct cggatgaactc gatgacnang ggcagctggt tgtgtntgat 240
 aaantccanc angttctcct tggtagacct cccttcaaag ttgttccggc ctcatcaaaa 300
 ctctcnnaan angannancc canctttgtc gagctggatc ttgganaaca cgtcactgtt 360
 ggaaactgat cccaaatggt atgtcatcca tcgctctgct tgccctgaaa aaacttgctt 420
 ggcncaaatc cgactcccn tccttgaaag aagccnatca cccccctc cctggactcc 480
 nncaangact ctncgcgtnc ccntccng cagggttggg ggcannccgg gccntgcgc 540
 ttcttcagcc agttcacnat nttcatcagc ccctctgcca gctgtntat tcttggggg 600
 ggaanccgtc tctcccttcc tgaannaact ttgaccgtng gaatagccgc gcntcncnt 660
 acntnctggg ccgggttcaa antccctcnn ttgcnntcn cctcgggcca ttctggattt 720
 necnaacttt tctcttccc cnccccncgg ngtttgntt tttcatnggg ccccaactct 780
 gctnttggcc antccctgg gggcntntan cnccccctnt ggtcccntng ggcc 834

<210> 36
 <211> 814
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc feature
 <222> (1)...(814)
 <223> n = A,T,C or G

<400> 36

cgngcgcgttt	ccngccgcgc	cccgtttcca	tgacnaagge	tcccttcang	ttaaatacnn	60
cctagnaaac	attaatgggt	tgtctacta	atacatcata	cnaaccagta	agcctgcccc	120
naacgccaac	tcaggccatt	cctaccaaag	gaagaaaggc	tggtctctcc	acccctgtga	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanagggttt	gttctcatgg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360
ggcttgatgg	tatcactgcc	acntttccac	ccagctgggc	ncctttcccc	catntttgtc	420
antganctgg	aaggcctgaa	nccttagctc	caaaagtctc	ngcccacaag	accggccacc	480
aggggaggtc	ntttncagtg	gatctgccaa	anantaccn	tatcatcnnt	gaataaaaag	540
gcccctgaac	ganatgcttc	cancancctt	taagacccat	aatcctngaa	ccatgggtgcc	600
cttccgggtct	gatecnaaag	gaatgttctt	gggtcccant	ccctcctttg	ttnccttacgt	660
tgtnttggac	ccntgctngn	atnacccaan	tganatcccc	ngaagcacc	tnccctggc	720
atgtganttt	cntaaattct	ctgcccactn	netgaaagca	cnattccctn	ggcnccnaan	780
gnggaactca	agaaggtctn	ngaaaaacca	cncn			814

<210> 37
 <211> 760
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(760)
 <223> n = A,T,C or G

<400> 37						
gcatgctgct	cttctcctcaa	gttgttcttg	ttgccataac	aaccaccata	ggtaaagcgg	60
gcgcagtgtt	cgctgaagg	gtttagtagt	cagcgcgga	tgctctcctt	gcagagtcc	120
gtgtctggca	gggtccacgca	atgccctttg	tactgggga	aatggatgcg	ctggagctcg	180
tcnaanccac	tcgtgtattt	ttcacangca	gcctcctccg	aagcctccgg	gcagttgggg	240
gtgtcgtcac	actccactaa	actgtcgatn	cancagccca	ttgctgcagc	ggaactgggt	300
gggctgacag	gtgccagaac	acactggatn	ggcctttcca	tggaagggcc	tgggggaaat	360
cncctnancc	caaaactgcct	ctcaaaaggcc	accttgcaca	ccccgacagg	ctagaaatgc	420
actcttcttc	ccaaaaggtag	ttgttcttgt	tgcccaagca	ncctccanca	aacccaaaanc	480
ttgcaaaaatc	tgctccgtgg	gggtcatnnn	taccanggtt	ggggaaaana	acccggcngn	540
ganccnccct	gtttgaatgc	naaggnaata	atcctcctgt	cttgcttggg	tggaanagca	600
caattgaact	gttaacnttg	ggccgngttc	cncnnggtgt	gtctgaaact	aatcacccgc	660
actggaaaaa	ggtangtgcc	ttccttgaat	tcccaaannt	ccccctngnt	tggtgnnttt	720
ctcctctncc	ctaaaaatcg	tnttcccccc	centanggcg			760

<210> 38
 <211> 724
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(724)
 <223> n = A,T,C or G

<400> 38						
tttttttttt	tttttttttt	tttttttttt	tttttaaaaa	ccccctccat	tgaatgaaaa	60
cttccnaaat	tgtccaaccc	cctcnnccaa	atnnccattt	ccgggggggg	gttccaaacc	120
caaattaatt	ttgganttta	aattaaatnt	tnattngggg	aanaanccaa	atgtnaagaa	180
aatttaaccc	attatnaact	taaatnccn	gaaaccntg	gnttccaaaa	atttttaacc	240
cttaaatccc	tccgaaattg	ntaanggaaa	accaaattcn	cctaaggctn	tttgaaggtt	300
ngatttaaac	ccccctnant	tnttttnacc	cnngnctnaa	ntatttngnt	tccggtgttt	360
tcctnttaan	cntnggtaac	tcccgnata	gaannnccct	aanccaatta	aaccgaattt	420
tttttgaatt	ggaaattccn	nggggaattna	ccgggggttt	tcccnttttg	gggccatncc	480
cccnctttcg	gggtttgggn	ntaggttgaa	tttttnnang	ncccaaaaaa	nccccccaana	540
aaaaaactcc	caagnnttaa	ttngaantnc	ccccctccca	ggccttttgg	gaaaggnggg	600
ttnttggggg	ccngggantt	cnttcccccn	ttncncccc	ccccccnggt	aaanggttat	660

ngnnttttgggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccgggncg 720
gccg 724

<210> 39
<211> 751
<212> DNA
<213> Homo sapien

<220>
<221> misc feature
<222> (1)...(751)
<223> n = A,T,C or G

<400> 39
tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120
tttattttatt ttactgaaa gtgagaggga actttttgtg ctttttttcc tttttctgta 180
ggccgcctta agctttctaa atttggaaca tctaagcaag ctgaanggaa aaggggggtt 240
cgcaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300
ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc ttttaattana 360
cttgggggtt ccctccccc accaaccccn ctgacaaaaa gtgccngccc tcaaatnatg 420
tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt ntcccccnc caggtnaaaa 480
tgaagggtta ccatntttta cncacactcc acntggcnnn gcctgaatcc tcnaaaancn 540
ccctcaancn aattnctnng ccccggtcnc gcntnngtcc cnccegggct cggggaantn 600
cacccccng annnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660
cnnagactnt cctcnnncn cncaattttc tttntntcac gaacncgnnc cnnaaaatgn 720
nnnnncctc cncnngtcn naatcnccan c 751

<210> 40
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc feature
<222> (1)...(753)
<223> n = A,T,C or G

<400> 40
gtggtatttt ctgtaagatc aggtgttcct ccctcgtagg tttagaggaa acaccctcat 60
agatgaaaac ccccccgaga cagcagcact gcaactgcca agcagccggg gtaggagggg 120
cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa 180
tggtctggaa gcgggcggtg tacctgcgta ggggcacacc gtcagggcc accaggaact 240
tctcaaagt ccaggcaacn tcgttgcgac acaccggaga ccaggtgatn agcttggggt 300
cggtcataan cgcggtggcg tcgtcgctgg gagctggcag ggcctccgc aggaaggcna 360
ataaaagggt cgcgcccgca ccgttcant cgcacttctc naanaccatg angttgggct 420
cnaaccacc accannccgg acttccctga nggaattccc aaatctcttc gntcttgggc 480
ttctnctgat gccctanctg gttgccnngn atgccaanca nccccaancc ccgggggtcct 540
aaancaccn cctcctcntt tcatctgggt tntntcccc ggacntgggt tcctctcaag 600
ggancccata tctcnaccn tactcacnt ncccccent gnnaccanc cttctanngn 660
tcccccccg ncctctggcc cntcaaanan gcttnacna cctgggtctg ccttcccccc 720
tncctatct gnacccnncn tttgtctcan tnt 753

<210> 41
<211> 341
<212> DNA
<213> Homo sapien

<400> 41
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaatg 60
agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120
ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gtaaaaaagt 180

tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tggtaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaattg	tgttttatat	attagggtag	t		341

<210> 42
 <211> 101
 <212> DNA
 <213> Homo sapien

<400> 42						
acttactgaa	tttagttctg	tgctcttcct	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcac	a		101

<210> 43
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 43						
acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttcctg	gtcctcacc	60
tccaggttg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaaccca	180
cctcttgaga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tggtacaga	acgagagtta	tcctggataa	ctcagagctg	agtacctgcc	cgggggcccgc	300
tcgaa						305

<210> 44
 <211> 852
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(852)
 <223> n = A,T,C or G

<400> 44						
acataaatat	cagagaaaag	tagtctttga	aatatttacg	tccaggaggt	ctttgtttct	60
gattatttgg	tgtgtgtttt	ggtttgtgtc	caaagtattg	gcagcttcag	ttttcatttt	120
ctctccatcc	tcgggcattc	ttcccaaatt	tatataccag	tcttcgtcca	tccacacgct	180
ccagaatttc	tctttttag	taatatctca	tagctcggtc	gagcttttca	taggtcatgc	240
tgctgttgtt	cttcttttta	ccccataget	gagccactgc	ctctgatttc	aagaacctga	300
agacgccctc	agatcggtct	tcccatttta	ttaatcctgg	gttcttgtct	gggttcaaga	360
ggatgtcgcg	gatgaattcc	cataagttag	tccctctcgg	gttgtgtctt	ttggtgtggc	420
acttggcagg	ggggtcttgc	tcttttttca	tatcagggtga	ctctgcaaca	ggaagggtgac	480
tggtggttgt	catggagatc	tgagcccggc	agaaagtgtt	gctgtccaac	aaatctactg	540
tgctaccata	gttgggtgtca	tataaatagt	tctngtcttt	ccagggtgttc	atgatggaag	600
gctcagtttg	ttcagttctg	acaatgacat	tgtgtgttga	ctggaacagg	tcactactgc	660
actggccgtt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccgggt	gaactcctgc	aaactcatgc	tgcaaagggtg	ctcgccgttg	atgtcgaaact	780
cntggaaagg	gatacaattg	gcattccagct	ggttggtgtc	caggaggtga	tggagccact	840
cccacacctg	gt					852

<210> 45
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 45						
acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttggacgaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggctggggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180

tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgacccg ctgt 234

<210> 46
 <211> 590
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(590)
 <223> n = A,T,C or G

<400> 46
 actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta 60
 atttgatagc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa 120
 aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa 180
 tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta 240
 aaagctttca aaanaanaaa ttattgcagt ctanttaatt caaacagtgt taaatgggat 300
 caggataaan aactgaaggg canaaagaat taattttcac ttcatgtaac ncacccanac 360
 ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc 420
 tggctctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag 480
 ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct 540
 gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

<210> 47
 <211> 774
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(774)
 <223> n = A,T,C or G

<400> 47
 acaagggggc ataatgaagg agtggggana gatttttaaag aaggaaaaaa aacgaggccc 60
 tgaacagaat tttcctgnac aacggggcct caaaataatt ttcttgggga ggttcaagac 120
 gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg 180
 cattacagac gggactctgg gaggaaggat aaacagaaaag gggacaaaag ctaatcccaa 240
 aacatcaaag aaaggaagggt ggcgtcatac ctcccagcct acacagttct ccagggtct 300
 cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg 360
 ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgat cctgctggc 420
 ccacactcct tgaacacaca tcccagggtt atattcctgg acatggctga acctcctatt 480
 cctaactccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540
 acggcatggg aagcctttct gacttgctg attactccag catcttgga caatccctga 600
 ttccccactc cttagaggca agataggggt gttaagagta gggctggacc acttgagacc 660
 aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct 720
 tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

<210> 48
 <211> 124
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(124)
 <223> n = A,T,C or G

<400> 48
 canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60
 ttgcaantat anaaatgtgt cataaattat aatgttctt aattacagct caacgcaact 120

tggt

124

<210> 49
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 49
 gccgatgcta ctatatttatt gcaggaggtg ggggtgtttt tattattctc tcaacagctt 60
 tgttggtaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120
 ttagggcacc catatcccaa gcantgt 147

<210> 50
 <211> 107
 <212> DNA
 <213> Homo sapien

<400> 50
 acattaaatt aataaaaagga ctggtggggt tctgctaaaa cacatggctt gatataattgc 60
 atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

<210> 51
 <211> 204
 <212> DNA
 <213> Homo sapien

<400> 51
 gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgacagg 60
 cgggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag 120
 gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcc 180
 cctccctttt ggaccagca atgt 204

<210> 52
 <211> 491
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(491)
 <223> n = A,T,C or G

<400> 52
 acaaagataa catttatctt ataacaaaaa tttgatagtt tttaaaggta gtattgtgta 60
 gggatatttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120
 ccatcagaca ggtttttaaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180
 aaaacttctt gtatcaattt cttttgttca aaatgactga cttantatt tttaaattatt 240
 tcanaaacac ttctcaaaa attttcaana tggtagcttt canatgtgcc ctcagtcca 300
 atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360
 atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat 420
 caattttatt tggataacaa aggggtctcca aattatattg aaaaataaat ccaagttaat 480
 atcactcttg t 491

<210> 53
 <211> 484
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(484)
 <223> n = A,T,C or G

<400> 53
 acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60
 gtattaacag ttgctgaagt ttgggtatit ttatgcagcat tttctttttg ctttgataac 120
 actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180
 caatcaaate tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct 240
 gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300
 agcttttgant ttctttgtgc tgatanggagg aaaggctgaa ttaccttggt gcctctccct 360
 aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420
 tanccttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc 480
 cant 484

<210> 54
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 54
 actaaacctc gtgcttgtga actccataca gaaaacgggtg ccatccctga acacggctgg 60
 ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag 120
 tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
 <211> 91
 <212> DNA
 <213> Homo sapien

<400> 55
 acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
 <211> 133
 <212> DNA
 <213> Homo sapien

<400> 56
 ggcggatgtg cggttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
 tggatttttg gtatctgtgg gttgggggga cgggtccagga accaataccc catggatacc 120
 aagggacaac tgt 133

<210> 57
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 57
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggegc 60
 gactgggagc tgagcccttc cctttgcgcc tgctcagag gattgttgcc gacntgcana 120
 tctcantggg ctggatncat gcagggt 147

<210> 58

<211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 58
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatfff ctgtatactc 60
 tgattacata catttatcct ttaaaaaaga tgtaaatcctt aatttttatg ccattctatta 120
 atttaccat gagttacctt gtaaatgaga agtcatgata gcaactgaatt ttaactagtt 180
 ttgacttcta agtttggt 198

<210> 59
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 59
 acaacaaatg gggtgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat 60
 ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt 120
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180
 tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagaccag 240
 cagaaggaat ctattttatac acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300
 tttcgtcttt attggacttc tttgaagagt 330

<210> 60
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 60
 accgtgggtg ccttctacat tcttgacggc tcttccacca acatctgggt ctacttcggc 60
 gtcgtgggct ccttctctct catctctatc cagctgggtg tgctcatcga ctttgccgac 120
 tcttggaacc agcgggtggct gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 61
 accccacttt tcttctgtg agcagtcctg acttctcact gctacatgat gaggggtgagt 60
 gggtgttgct.cttcaacagt atctccctt ttccggatct gctgagccgg acagcagtgc 120
 tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62
 <211> 30
 <212> DNA
 <213> Homo sapien

<400> 62
 cgctcgagcc ctatagttag tcgtattaga 30

<210> 63
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 63

acaagtcatt tcagcacccct ttgctcttca aaactgacca tcttttatat ttaatgcttc 60
ctgtatgaat aaaaatggtt atgtcaagt 89

<210> 64
<211> 97
<212> DNA
<213> Homo sapien

<400> 64
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60
aatcagtgca tccaggattg gtccttgat ctgggggt 97

<210> 65
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc feature
<222> (1)...(377)
<223> n = A,T,C or G

<400> 65
acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccct tttgatggca 60
gcatggcgtc ctaggccttg acacagcggc tggggtttgg gctntccaa accgcacacc 120
ccaacccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa 240
ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaaccg 300
tgggggtgaa ctaccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
ggcggggagg agcatgt 377

<210> 66
<211> 305
<212> DNA
<213> Homo sapien

<400> 66
acgcctttcc ctcagaattc agggaagaga ctgtgcctg ccttctccg ttgttgcgtg 60
agaacccgtg tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
aggaactaac tgcacctgg tctctcccc agtccccagt tcacctoca tccctcacct 180
tctccactc taaggatat caacactgcc cagcacagg gcctgaatt tatgtggtt 240
ttatatattt ttttaataaga tgcactttat gtcattttt aataaagtct gaagaattac 300
tgttt 305

<210> 67
<211> 385
<212> DNA
<213> Homo sapien

<400> 67
actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60
ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120
cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tctttagagg 240
ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360
catagtttct gtgctagtgg accgt 385

<210> 68
<211> 73
<212> DNA
<213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(536)
 <223> n = A,T,C or G

<400> 69
 actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctctgcagc 60
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300
 actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360
 ccgaaccata tgtaccaagt cccagcccaa cttggacacc tgtgccttcc atgaacagcc 420
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca 480
 gaangtcctt gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 70
 atgaccccta acagggggccc tctcagccct cctaattgacc tccggcctag ccatgtgatt 60
 tcacttccac tccataacgc tcctcatact aggcctacta accaaccacac taaccatata 120
 ccaatgatgg cgcgatgtaa cagcagaaag cacataccaa ggccaccaca caccacctgt 180
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
 agggattttt ctgagccttt taccactcca gcctagcccc taccctccaa ctaggagggc 300
 actggccccc aacaggcatc accccgctaa atcccttaga agtcccactc ctaaaccacat 360
 ccgtattact cgcatacagga gtatcaatca cctgagctca ccatagtcta atagaaaaa 420
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(533)
 <223> n = A,T,C or G

<400> 71
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattggttta 120
 tgtgatttta gtggtatttt tggcaccctt atatatgttt tccaaacttt cagcagtgat 180
 attattttcca taacttaaaa agtgagtgtg aaaaagaaaa tctccagcaa gcatctcatt 240
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300
 aaataggtgt gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
 cttcgtaatt ttggagtang aggttccctc ctcaattttg tattttttaa aagtacatgg 480
 taaaaaaaaa aattcacaac agtatataag gctgtaaaaat gaagaattct gcc 533

<210> 72

<211> 511
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72

tattacggaa	aaacacacca	cataattcaa	ctancaaaga	anactgcttc	agggcggtga	60
aatgaaagg	cttccaggca	gttatctgat	taaagaacac	taaaagagg	acaaggctaa	120
aagccgcagg	atgtctacac	tatancaggc	gctatttggg	ttggctggag	gagctgtgga	180
aaacatggan	agattgggtc	tgganacgc	cgtggctatt	cctcattgtt	attacanagt	240
gaggttctct	gtgtgcccac	tggtttgaaa	accgttctnc	aataatgata	gaatagtaca	300
cacatgagaa	ctgaaatggc	ccaaacccag	aaagaaagcc	caactagatc	ctcagaanac	360
gcttctaggg	acaataaccg	atgaagaaaa	gatggcctcc	ttgtgcccc	gtctgttatg	420
atttctctcc	attgcagcna	naaacccggt	cttctaagca	aacncagggtg	atgatggcna	480
aaatacaccc	cctcttgaag	naccnggagg	a			511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73

cagtgccagc	actggtgcc	gtaccagtac	caataacagt	gccagtgcc	gtgccagcac	60
cagtgggtgc	ttcagtgtg	gtgccagcct	gaccgccact	ctcacatttg	ggctcttcgc	120
tggtcttggt	ggagctggg	ccagcaccag	tggtcagctct	gggtgcctgtg	gtttctccta	180
caagtgaagt	tttagatatt	gttaatcctg	ccagtctttc	tcttcaagcc	aggtgcatc	240
ctcagaaacc	tactcaacac	agcactctag	gcagccacta	tcaatcaatt	gaagtgtgaca	300
ctctgcatta	aatctatttg	ccatttctga	aaaaaaaaaa	aaaaaaagg	cggtccgtcg	360
antctagagg	gcccgtttta	accgcgtgat	cagcctcgac	tgtgccttct	anttgcacgc	420
catctgttgt	ttgccctcc	cccngtgctt	tctttgacct	tggaaagtgc	cactcccact	480
gtcctttcct	aantaaaat					499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74

tttcatagga	gaacacactg	aggagatact	tgaagaattt	ggattcagcc	gcgaagagat	60
ttatcagctt	aactcagata	aaatcattga	aagtaataag	gtaaaagcta	gtctctaact	120
tccaggccca	cggctcaagt	gaatttgaat	actgcattta	cagtgtagag	taacacataa	180
cattgtatgc	atggaaacat	ggaggaacag	tattacagt	tcttaccact	ctaatcaaga	240
aaagaattac	agactctgat	tctacagtga	tgattgaatt	ctaaaaatgg	taatcattag	300
ggcttttgat	ttataanact	ttgggtactt	atactaaatt	atggtagtta	tactgccttc	360
cagtttgctt	gatataattg	ttgatattaa	gattcttgac	ttatatattg	aatgggttct	420
actgaaaaan	gaatgatata	ttcttgaaga	catcgatata	catttattta	cactcttgat	480
tctacaatgt	agaaaatgaa	ggaaatgccc	caaattgtat	ggtgataaaa	gtccccgt	537

<210> 75
 <211> 467
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(467)
 <223> n = A,T,C or G

<400> 75
 caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
 tgcataattac acgtacctcc tcctgtccct caagtagtgt ggtctatttt gccatcatca 120
 cctgtctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
 tggcacaagg aggccatctt ttctcatcgc gttattgtcc ctagaagcgt cttctgagga 240
 tctagttggg ctttctttct gggtttgggc catttcantt ctcattgtgt tactattcta 300
 tcattattgt ataacggttt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
 caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 76
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcgtac 60
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120
 atccagcaga gaatggaaa tcaaatttcc tgaattgcta tgtgtctggg tttcatccat 180
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
 acttgtcttt cagcaaggac tgggtctttct atctcttgta ctacactgaa ttcaccccca 300
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
 tttagtgagg tccanacatg taagcagcan catgggaggt 400

<210> 77
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 77
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgtgct 120
 caggcactgt tcatctcagc ttttctgtcc ctttgcctcc ggcaagcgtc tctgctgaaa 180
 gttcatatct ggagcctgat gtcttaacga ataaaggctc catgctccac ccgaaaaaaa 240
 aaaaaaaa 248

<210> 78
 <211> 201
 <212> DNA
 <213> Homo sapien

<400> 78
 actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60
 tcaccagac cccgccctgc ccgtgcccac cgctgctgct aacgacagta tgatgcttac 120
 tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct 180
 gatttaaaaa aaaaaaaaaa a 201

<210> 79
 <211> 552
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(552)
 <223> n = A,T,C or G

<400> 79
 tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120
 cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240
 atgcaagtta gtaattactc aggggttaact aaattacttt aatatgctgt tgaacctact 300
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta 420
 ttcccaggaa tatggggttc atttatgaat antacccggg anagaagttt tgantnaaac 480
 cngttttggt taatacgta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540
 aaaaaaaaaa aa 552

<210> 80
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 80
 acaggggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60
 ggggaaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240
 aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300
 tcttctaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc 360
 tcttggtttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420
 gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

<400> 81
 tttttttttg tatgcctcn ctgtggngtt attgttgctg ccaccctgga ggagcccagt 60
 ttcttctgta tttttctttt ctggggggtc ttccctggtc tgccctccca ttcccagcct 120
 ctcatccca tcttgactt ttgctagggt tggaggcgt ttccctggtag cccctcagag 180
 actcagtcag cgggaataag tcctaggggt ggggggtgtg gcaagccggc ct 232

<210> 82
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 82
 aggcgggagc agaagctaaa gccaaagccc aagaagagtgc gcagtgccag cactgggtgcc 60
 agtaccagta ccaataacat gccagtgccag gtgccagcac cagtgggtggc ttcagtgtctg 120
 gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggt ggagctgggtg 180
 ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtggatg tttagatatt 240
 gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300
 agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360
 ccatttcaaa aaaaaaaaaa aaa 383

<210> 83
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

<400> 83
 accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca 60
 gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgctcagc 120
 ccacctgctc cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180
 acgcttcaag gtgctcatga cccagcaacc gcgcctgtc ctctgagggt ccttaaaactg 240
 atgtcttttc tgccacctgt taccctcctg agactccgta accaaaactct tcggactgtg 300
 agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat 360
 tatgcttggtg tgaggcaatc atgggtggcat caccatnaa gggaacacat ttganttttt 420
 tttcncatat tttaaattac naccagaata ntccagaata aatgaattga aaaactctta 480
 aaaaaaaaaa aaaa 494

<210> 84
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 84
 gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60
 agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
 gaggacatgg acgtggccct catggagcac agcaactgct cgctggagcc cggcttcttg 180
 gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctgggtg 240
 gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctgggtcac ttgctcattg 300
 ccattgtcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
 agcgttnccg cctcatccgg 380

<210> 85
 <211> 481
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(481)

<223> n = A,T,C or G

<400> 85

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cctcctgcat	cttggggcgg	ctaatatcca	120
ggaaactctc	aatcaagtca	ccgtcnatna	aacctgtggc	tggttctgtc	ttccgctcgg	180
tgtgaaagga	tctccagaag	gagtgtcga	tcttccccac	acttttgatg	actttattga	240
gtcgattctg	catgtccagc	aggaggttgt	accagctctc	tgacagtgag	gtcaccagcc	300
ctatcatgcc	nttgaacgtg	ccgaagaaca	ccgagccttg	tgtggggggt	gnagtctcac	360
ccagattctg	cattaccaga	nagccgtggc	aaaaganatt	gacaactcgc	ccaggnggaa	420
aaagaacacc	tcttggaagt	gctngccgct	cctcgtcctt	tggtggnggc	gcntnccctt	480
t						481

<210> 86

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 86

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgctg	agaattcatt	60
acttgaaaa	gcaacttnaa	gcctggacac	tggtattaaa	attcacaata	tgcaacactt	120
taaacagtgt	gtcaatctgc	tcccttactt	tgatcatcacc	agtctgggaa	taaggggtatg	180
ccctattcac	acctgttaaa	agggcgctaa	gcatttttga	ttcaacatct	ttttttttga	240
cacaagtccg	aaaaaagcaa	aagtaaacag	ttnttaattt	gttagccaat	tcactttctt	300
catgggacag	agccatttga	tttaaaaaag	aaattgcata	atattgagct	ttgggagctg	360
atatntgagc	ggaagantag	cctttctact	tcaccagaca	caactccttt	catattggga	420
tgttnacnaa	agttatgtct	cttacagatg	ggatgctttt	gtggcaattc	tg	472

<210> 87

<211> 413

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(413)

<223> n = A,T,C or G

<400> 87

agaaaccagt	atctctnaaa	acaacctctc	ataccttgtg	gacctaat	ttgtgtgcgtg	60
tgtgtgtgcg	cgcatattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctcttttgt	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180
ttgtcttctg	tgtaaatggt	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgac	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	cttgactagg	300
ggggacaaaag	aaaagcanaa	ctgaacatna	gaaacaattn	cctgggtgaga	aattncataa	360
acagaaattg	ggtngtatat	tgaananng	catcattnaa	acgttttttt	ttt	413

<210> 88

<211> 448

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(448)

<223> n = A,T,C or G

<400> 88
 cgcagcgggt cctctctatc tagctccagc ctctcgctg cccactccc cgcgtcccgc 60
 gtcctagccn accatggccg ggcccctgcg cgcgccgctg ctccctgctg ccatacctggc 120
 cgtggccctg gccgtgagcc ccgcggccgg ctccagtcct ggcaagccgc cgcgcctggt 180
 gggaggccca tggaccccg cgtggaagaag aagggtgtgc gcgtgcactg gactttgccg 240
 tcggcnanta caacaaacc gcaacnactt ttaccnagcn cgcgtgcag gttgtgccg 300
 cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctg gccaaacnng 360
 tttaccagaa ccnagccaat tngaacaatt ncccctccat aacagcccct tttaaaaagg 420
 gaancantcc tgntcttttc caaat ttt 448

<210> 89
 <211> 463
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(463)
 <223> n = A,T,C or G

<400> 89
 gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60
 gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120
 agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt 180
 ctcaagtaca agttntttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240
 tttnatgttn agacttgccct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtg 300
 ttttaacaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360
 aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420
 aattcnnana anttcagntn tcatacaaca naacngganc ccc 463

<210> 90
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 90
 agggattgaa ggtctntnt actgtcggac tgttcancca ccaactctac aagttgctgt 60
 ctccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaat 120
 tcttcaccag tcacatcttc taggacctt ttggattcag ttagtataag ctcttccact 180
 tctttgtta agacttcac tggtaaagtc ttaagtttg tagaaaggaa ttaattgct 240
 cgttctctaa caatgtcctc tccttgaagt atttggtga acaaccacc tnaagtcct 300
 ttgtgcatcc attttaaata tacttaatag ggcattggt cactagggtt aattctgcaa 360
 gagtcatctg tctgcaaaag ttgcgttagt atatctgcca 400

<210> 91
 <211> 480
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(480)
 <223> n = A,T,C or G

<400> 91
 gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60

```

ggctctacccc acatggggagc agcatgccgt agntatataa ggctattccc tgagtcagac      120
atgcctctttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nncgcgtctt      180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaat tcacccacga      240
gacacttgaa aggtgtaaca aagcgactct tgcatgtgtt tttgtccctc cggcaccagt      300
tgtcaatact aaccgcgtgg tttgcctcca tcacatttgt gatctgtagc tctggatata      360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt      420
ngatcagggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa      480

```

```

<210> 92
<211> 477
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

```

```

<400> 92
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact      60
ggctcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt      120
cccacgcagg cagcagcggg gccgggtcaat gaactccact cgtggcttgg ggttgacggg      180
taantgcagg aagagggtga ccacctcgcg gtccaccagg atgcccgact gtgcgggacc      240
tgcagcgaaa ctctcgtatg gtcattgagcg ggaagcgaat gangcccagg gccttgccca      300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg      360
accagcggac aaacggcggt gaacagccgc acctcacgga tgcccantgt gtgcgcgtcc      420
aggaacggcn ccagcgtgtc caggtcaatg tcggtgaanc ctccgcgggt aatggcg      477

```

```

<210> 93
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

```

```

<400> 93
gaacggctgg acctgcctc gcattgtgct gctggcagga ataccttggc aagcagctcc      60
agtcgcagca gcccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc      120
cgcttcaatg cagaaccant agtgggagca ctgtgtttag agttaagagt gaacactgtn      180
tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaata ttccaaacaa      240
caacaacaaa ataactgtt tgctgtttna gttgtataaa agtangtgat tctgtatnta      300
aagaaaatat tactgttaca tatactgctt gcaanttctg tatttattgg tnctctggaa      360
ataaatatat tattaata

```

```

<210> 94
<211> 495
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(495)
<223> n = A,T,C or G

```

```

<400> 94
ccctttgagg ggttaggggc cagttcccag tggaagaaac aggccaggag aantgcgtgc      60
cgagctgang cagatttccc acagtgacct cagagccctg ggctatagtc tctgacctc      120
ccaaggaaa accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg      180
gaaggcccca ttccggggct gttccccgag gaggaaggga aggggctctg tgtgcccccc      240

```

```

acgaggaana ggccctgant cctgggatca nacacccctt cacgtgtatc cccacacaaa 300
tgcaagctca ccaaggtccc ctctcagtc cttccctaca ccctgaacgg ncaactggccc 360
acacccaccc agancancca cccgccatgg ggaatgttct caaggaatcg cngggcaacg 420
tggactctng tcccnaagg gggcagaatc tccaatagan gganngaacc cttgctnana 480
aaaaaaaaa aaaaa 495

```

```

<210> 95
<211> 472
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 95
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
cctctggaag ccttgcgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
tagctgtttt gagttgattc gcaccactgc accacaactc aatatgaaa ctatttnact 180
tatttattat cttgtgaaa gtatacaatg aaaattttgt tcatactgta tttatcaagt 240
atgatgaaaa gcaatagata tatattcttt tattatgttn aattatgatt gccattatta 300
atcggaacaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac 360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata 420
tttanttcan taatttcttt ccttgtttac gtttaattttg aaaagaatgc at 472

```

```

<210> 96
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc feature
<222> (1)...(476)
<223> n = A,T,C or G

```

```

<400> 96
ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat 60
gtgggtgaaat ttcaaaatta tatgtaactt ctactagttt tactttctcc cccaagtctt 120
ttttaactca tgattttttac acacacaatc cagaacttat tatatagcct ctaagtcttt 180
attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcanaatg ttctagntat 240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naacccaaat 300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct 360
gcagggtactc ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt 420
tacaaagtct atcttctctca nangtctgtt aaggaacaat ttaatcttct agcttt 476

```

```

<210> 97
<211> 479
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc feature
<222> (1)...(479)
<223> n = A,T,C or G

```

```

<400> 97
actcttttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaatggata 60
aaataatgct gcaaacttaa tgttcttatg caaaatggaa cgctaataa acacagctta 120
caatcgcaaa tcaaaactca caagtgtctca tctgtttag atttagtgta ataagactta 180
gattgtgctc cttcggatat gattgtttct canatcttg gcaatnttcc ttagtcaaat 240
caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt 300

```

gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat	360
ntnnnttttta natcaaagta ttttgtgttt ggaantgttn aaatgaaatc tgaatgtggg	420
ttcnatctta ttttttcccn gacnactant tnttttttta gggncatttc tganccatc	479

<210> 98
 <211> 461
 <212> DNA
 <213> Homo sapien

<400> 98	
agtgaattgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta	60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgattcag ttctctctac ggatgagaga ctggctcaag aatatectca tgcagcttta	240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat	300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct ctttaaggact	360
ttaagaaaaa ctaccacatg ttgtgtatcc tggcgccggc cgtttatgaa ctgaccaccc	420
tttgaataa tcttgacgct cctgaacttg ctccctctgcg a	461

<210> 99
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 99	
gtggcgcgcg gcaggtgttt cctcgtagcg cagggccccc tcccttcccc aggcgtccct	60
cggcgccctc gcgggcccga ggaggagcgg ctggcggggtg gggggagtgt gaccacccct	120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c	171

<210> 100
 <211> 269
 <212> DNA
 <213> Homo sapien

<400> 100	
cgcccgcaag tgcaactcca gctggggcgg tgcggacgaa gattctgcca gcagttgggc	60
cgactgcgac gacggcgggc ggcacagtcg caggtgcagc gcggggcgcc ttgggtcttg	120
aaggctgagc tgacgcccga gaggtcgtgt caggtcccac gacctgacg ccgtcgggga	180
cagccggaac agagcccggt gaagcgggag gcctcgggga gcccctcggg aaggcgggcc	240
cgagagatac gcaggtgcag gtggccgcc	269

<210> 101
 <211> 405
 <212> DNA
 <213> Homo sapien

<400> 101	
tttttttttt ttttgaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca	60
gctagcaagg taacagggtg gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg	120
ttgattgggt tgtctttatg ggggcggggt ggggtagggt aaacgaagca aataacatgg	180
agtgggtgca ccctccctgt agaacctggt tacaagctt ggggcagttc acctgggtctg	240
tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatattcttt agagagtcca	300
ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagtgtg	360
gatgatcagt acgaataccg aggcataatc tcatatcggt ggcca	405

<210> 102
 <211> 470
 <212> DNA
 <213> Homo sapien

<400> 102	
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	60

ggcacttaat	ccatttttat	ttcaaaatgt	ctacaaatth	aatcccatta	tacgggtattt	120
tcaaaatcta	aattattcaa	attagccaaa	tccttaccaa	ataataccca	aaaatcaaaa	180
atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atatatacgg	ctgggtgtttt	240
caaagtacaa	ttatcttaac	actgcaaaaca	ttttaaggaa	ctaaaataaa	aaaaaacact	300
ccgcaaaggt	taaaggggaa	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	ttactcact	ttgtttattt	420
ttttaaacca	ttgtttgggc	ccaacacaat	ggaatccccc	ctggactagt		470

<210> 103
 <211> 581
 <212> DNA
 <213> Homo sapien

<400> 103	
tttttttttt	ttttttttga
tacacatatt	tattttataa
taaatggaaa	ctgccttaga
gaaaatcttc	tctagctctt
atcttctctg	tctttaaaat
gcttctctag	cctcatttcc
agggaaaaca	ggaagagaaa
acgttaataa	aatagcattt
ccattttagt	cactaaacga
tcaaaagcta	atataagata
ccccctctt	ataaaaaaca
atattcaaaa	ggcagctttt
ttaggaatta	gcttaaaatc
atttttgact	cttgtaaaac
ttccattttt	tccctattcc
ctactattag	taagtggctt
ttatattcat	atttctacct
gctcaaaaga	aggcttagat
ccagaatgca	aaaggtttgt
tcattctttct	g
	60
	120
	180
	240
	300
	360
	420
	480
	540
	581

<210> 104
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 104	
tttttttttt	tttttttttt
cactctctag	atagggcatg
ctcttatgct	atatcatatt
aggaaatctg	ttcattcttc
gagggttttc	ttctctattt
ttcatgcaaa	ctagaaaata
caaaactgct	caaattgttt
aaatcacatt	tacgacagca
aaaggaaacat	ttttagcctg
tgaattcaca	tggtattatt
ttttttctct	cttttttttt
atctttccag	cttttaaaata
ctaatgagtc	actggcttat
agtactacct	tgcatattga
atttgatca	aacctttatt
atagcatta	gagctaatac
ggtataatta	gctaaattcac
cacaatgg	
	60
	120
	180
	240
	300
	360
	420
	480
	540
	578

<210> 105
 <211> 538
 <212> DNA
 <213> Homo sapien

<400> 105	
tttttttttt	tttttcagta
gaaaagtgcc	ttacatttaa
gtcttggaaca	ccaattattaa
aagatcatag	agcttgtaag
aaatccacta	ttagcaaaata
ggggtgtcac	tggtaaacca
tgtactttgc	taatacgtgg
ggcgagaaat	gaggaagaaa
agatatgttt	cctttgcmaa
caatatttat	ttttatattt
tttctcaaag	tgatcagagg
atacaccaaa	atacattaag
aaatttgacc	tcagaaactc
gacttcttgc	tttaattttg
tacttagtga	tagattctta
ctttcttcaa	tcttttaagg
gttctttcta	tggaaggatt
ttactactag	tgaaaccc
	60
	120
	180
	240
	300
	360
	420
	480
	538

<210> 106
 <211> 473
 <212> DNA
 <213> Homo sapien

<400> 106
 tttttttttt ttttttagtc aagtttctat ttttattata attaaagtct tggtcatttc 60
 atttattagc tctgcaactt acatatttta attaaagaaa cgtttttagac aactgtacaa 120
 tttataaatg taagggtgcc tttattgagta atatattcct ccaagagtgg atgtgtccct 180
 tctcccacca actaatgaac agcaacatta gtttaatttt attagtagat atacactgct 240
 gcaaacgcta attctcttct ccatcccat gtgatattgt gtatatgtgt gagttggtag 300
 aatgcatcac aatctacaat caacagcaag atgaagctag gctgggcttt cggtgaaaat 360
 agactgtgtc tgtctgaatc aaatgatctg acctatcctc ggtggcaaga actcttcgaa 420
 ccgcttcctc aaaggcgctg ccacatttgt ggctctttgc acttgtttca aaa 473

<210> 107
 <211> 1621
 <212> DNA
 <213> Homo sapien

<400> 107
 cgccatggca ctgcagggca tctcggtcat ggagctgtcc ggcctggccc cgggcccgtt 60
 ctgtgctatg gtctggctg acttcggggc gcgtgtggta cgcgtggacc ggcccggctc 120
 ccgctacgac gtgagccgct tgggcccggg caagcgctcg ctagtgctgg acctgaagca 180
 gccgcgggga gccgccgtgc tgcggcgctc gtgcaagcgg tcggatgtgc tgcgtggagcc 240
 cttccgcgcg ggtgtcatgg agaaactcca gctgggcccga gagattctgc agcgggaaaa 300
 tccaaggcctt atttatgccca ggctgagtgg atttggccag tcaggaagct tctgcccgtt 360
 agctggccac gatatcaact atttggcttt gtccaggtgtt ctctcaaaaa ttggcagaag 420
 tgggtgagaat ccgtatgccc cgtggaatct cctggctgac tttgctggtg gtggccttat 480
 gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgcactgaca agggtcaggt 540
 cattgatgca aatatggtgg aaggaacagc atattttaagt tcttttctgt ggaaaactca 600
 gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
 ctatacgact taecaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
 gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat 780
 gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
 gaaggcagag tgggtgtcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
 ttttgaggag gttgttcatc atgatcacia caaggaacgg ggctcgttta tcaccagtga 960
 ggagcaggac gtgagccccc gccctgcacc tctgctggtt aacaccccag ccateccttc 1020
 tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt 1080
 cagccgcgaa gagatttatc agcttaactc agataaaatc attgaaagta ataaggtaaa 1140
 agctagtctc taacttccag gccacaggct caagtgaatt tgaatactgc atttacagt 1200
 tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
 ccactctaata caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa 1320
 aatgggttatc attagggctt ttgatttata aaactttggg tacttatact aaattatggt 1380
 agttattctg ccttccagtt tgcctgatat atttgttgat attagattc ttgacttata 1440
 ttttgaatgg gttctagtga aaaaggaatg atatattcct gaagacatcg atatacattt 1500
 atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatggtgat 1560
 aaaagtcacg tgaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
 a 1621

<210> 108
 <211> 382
 <212> PRT
 <213> Homo sapien

<400> 108
 Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1 5 10 15
 Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20 25 30
 Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35 40 45
 Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50 55 60
 Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65 70 75 80

Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85 90 95
 Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
 100 105 110
 Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
 115 120 125
 Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
 130 135 140
 Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
 145 150 155 160
 Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
 165 170 175
 Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
 180 185 190
 Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
 195 200 205
 Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
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 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

<210> 109

<211> 1524

<212> DNA

<213> Homo sapien

<400> 109

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cgcgagtagc	aacagcgcc	gaaagtgtg	gagcgggagg	tccagcagt	tagccgcgtc	1080
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<210> 110

<211> 3410

<212> DNA

<213> Homo sapien

<400> 110

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<210> 111
 <211> 1289
 <212> DNA
 <213> Homo sapien

<400> 111						
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ccatgcagtg	cttcagcttc	attaagacca	tgatgatcct	cttcaatttg	ctcatctttc	180
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tgttacaatg	ttaaaaaaa	aaaaaaaaa				1289

<210> 112
 <211> 315
 <212> PRT
 <213> Homo sapien

<400> 112															
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Leu	Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe
			20					25					30		
Phe	Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala
		35				40					45				
Thr	Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu
		50			55						60				
Arg	Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro
65				70					75					80	
Gln	Glu	Asp	Met	Asp	Val	Ala	Leu	Met	Glu	His	Ser	Asn	Cys	Ser	Ser
			85					90					95		
Glu	Pro	Gly	Phe	Trp	Ala	His	Pro	Pro	Gly	Ala	Gln	Ala	Gly	Thr	Cys
			100				105						110		
Val	Ser	Gln	Tyr	Ala	Asn	Trp	Leu	Val	Val	Leu	Leu	Leu	Val	Ile	Phe

115	120	125
Leu Leu Val Ala Asn Ile	Leu Leu Val Asn Leu	Leu Ile Ala Met Phe
130	135	140
Ser Tyr Thr Phe Gly Lys	Val Gln Gly Asn Ser	Asp Leu Tyr Trp Lys
145	150	155
Ala Gln Arg Tyr Arg	Leu Ile Arg Glu Phe	His Ser Arg Pro Ala Leu
165	170	175
Ala Pro Pro Phe Ile Val	Ile Ser His Leu Arg	Leu Leu Leu Arg Gln
180	185	190
Leu Cys Arg Arg Pro Arg	Ser Pro Gln Pro Ser	Ser Pro Ala Leu Glu
195	200	205
His Phe Arg Val Tyr Leu	Ser Lys Glu Ala Glu	Arg Lys Leu Leu Thr
210	215	220
Trp Glu Ser Val His Lys	Glu Asn Phe Leu Leu	Ala Arg Ala Arg Asp
225	230	235
Lys Arg Glu Ser Asp Ser	Glu Arg Leu Lys Arg	Thr Ser Gln Lys Val
245	250	255
Asp Leu Ala Leu Lys Gln	Leu Gly His Ile Arg	Glu Tyr Glu Gln Arg
260	265	270
Leu Lys Val Leu Glu Arg	Glu Val Gln Gln Cys	Ser Arg Val Leu Gly
275	280	285
Trp Val Ala Glu Ala Leu	Ser Arg Ser Ala Leu	Leu Pro Pro Gly Gly
290	295	300
Pro Pro Pro Pro Asp Leu	Pro Gly Ser Lys Asp	315
305	310	

<210> 113
 <211> 553
 <212> PRT
 <213> Homo sapien

<400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
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Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
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Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
35 40 45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
50 55 60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65 70 75 80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
85 90 95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
100 105 110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
115 120 125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130 135 140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145 150 155 160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
165 170 175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
180 185 190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
195 200 205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
210 215 220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

<210> 114
 <211> 241
 <212> PRT
 <213> Homo sapien

<400> 114
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 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys

115	120	125
Asp Tyr Gly Ser Gln Glu	Asp Phe Thr Gln Val	Trp Asn Thr Thr Met
130	135	140
Lys Gly Leu Lys Cys Cys	Gly Phe Thr Asn Tyr	Thr Asp Phe Glu Asp
145	150	155
Ser Pro Tyr Phe Lys Glu	Asn Ser Ala Phe	Pro Pro Phe Cys Cys Asn
165	170	175
Asp Asn Val Thr Asn Thr	Ala Asn Glu Thr Cys Thr	Lys Gln Lys Ala
180	185	190
His Asp Gln Lys Val Glu	Gly Cys Phe Asn Gln	Leu Leu Tyr Asp Ile
195	200	205
Arg Thr Asn Ala Val Thr	Val Gly Gly Val Ala	Ala Gly Ile Gly Gly
210	215	220
Leu Glu Leu Ala Ala Met	Ile Val Ser Met Tyr	Leu Tyr Cys Asn Leu
225	230	235
Gln		240

<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

<400> 115
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 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180
 actggtagaa aaacatctga agagctagtc tatcagcatc tgacaggtga attggatggg 240
 tctcagaacc atttcacca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300
 tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360
 ttagtc 366

<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 116
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 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120
 agactttact attttcatat tttaagacac atgattttatc ctatttttagt aacctggttc 180
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240
 tcaatctnga actatctana tcacagacat ttctatttctt tt 282

<210> 117
 <211> 305
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(305)
 <223> n = A,T,C or G

<400> 117
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 tatttatcct cctccttgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120

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aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga 180
tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt 240
gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
tgggt 305

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<210> 118
<211> 71
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(71)
<223> n = A,T,C or G

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<400> 118
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aantcctggg t 71

```

```

<210> 119
<211> 212
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(212)
<223> n = A,T,C or G

```

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<400> 119
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gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctactaanc ggaattaant 180
aatggantca aganactccc aggcctcagc gt 212

```

```

<210> 120
<211> 90
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

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<400> 120
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctcttgcc 60
ctccgccggc gcagaacatg ctgggggtgg 90

```

```

<210> 121
<211> 218
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

```

```

<400> 121
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gaataagatt tgctaaaaga ttgggggcta aaacatgggt attgggagac atttctgaag 120

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atatncangt aaattangga atgaattcat ggttcctttg ggaattcctt tacgatngcc 180
agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122
<211> 171
<212> DNA
<213> Homo sapien

<400> 122
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60
catttgtag ctcatggaac aggaagtcgg atgggtgggc atcttcagtg ctgcatgagt 120
caccaccccg gcggggtcac ctgtgccaca ggtccctgtt gacagtgcgg t 171

<210> 123
<211> 76
<212> DNA
<213> Homo sapien

<220>
<221> misc feature
<222> (1) ... (76)
<223> n = A,T,C or G

<400> 123
tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca ttattatca 60
ttatcaanta ttgtgt 76

<210> 124
<211> 131
<212> DNA
<213> Homo sapien

<400> 124
acctttcccc aaggccaatg tctgtgtgc taactggccg gctgcaggac agctgcaatt 60
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120
ttaagatttg t 131

<210> 125
<211> 432
<212> DNA
<213> Homo sapien

<400> 125
actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg 60
cttgaaaaag aggtgatagc tcttcagagg acttgtagact ttgtctcaga tgctgaagaa 120
ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240
ctcttgaagt atcagtcact ttgagaatg tttcttagtt actgcatact tcatggatcc 300
catgggtggg gtcttgcac tgtaagaatg gaattgattt tgcttttgca agaattctcag 360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaacctc agtgcctctc 420
ctctttgctt gt 432

<210> 126
<211> 112
<212> DNA
<213> Homo sapien

<400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt 112

<210> 127

<211> 54
 <212> DNA
 <213> Homo sapien

<400> 127
 accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
 <211> 323
 <212> DNA
 <213> Homo sapien

<400> 128
 acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120
 ttctctctga agtctaggtt acccattttg gggacccatt ataggcaata aacacagttc 180
 ccaaagcatt tggacagttt cttgttggtt tttagaatgg ttttcctttt tcttagcctt 240
 ttctgcataa aggtcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct 300
 aggtgcctt cttttccatg tcc 323

<210> 129
 <211> 192
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(192)
 <223> n = A,T,C or G

<400> 129
 acatacatgt gtgtatatatt ttaaataatca cttttgtatc actctgactt tttagcatac 60
 tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120
 tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180
 gataaacaaa gt 192

<210> 130
 <211> 362
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(362)
 <223> n = A,T,C or G

<400> 130
 ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60
 tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa 120
 gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa 180
 ttctgtattc catttttgta acgcttggt gatgtaacct gctangaggc taactttata 240
 cttatttaaa agctcttatt ttgtggtcat taaaatggca atttatgtgc agcactttat 300
 tgcagcagga agcacgtgtg gggttggtgt aaagctcttt gctaattcta aaaagtaatg 360
 gg 362

<210> 131
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131

ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca	60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga	120
gtttctccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc	180
ttctgaacta gattaaggca gcttgtaaatt ctgatgtgat ttggttttatt atccaactaa	240
cttccatctg ttatcactgg agaaagccca gactcccccac gacnggtacg gattgtgggc	300
atanaaggat tgggtgaagc tggcgttgtg gt	332

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132

acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctagggtgtcc	60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat	120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt	180
tttagcaagt taaaatgaan atgacaggaa aggccttatt atcaacaaag agaagagttg	240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct aggggaagcct	300
gtaacaatct acaattggtc ca	322

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133

acaagccttc acaagttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt	60
cttggttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta	120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg	180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt	240
cccacgaaac actaataaaa accacagaga ccagcctg	278

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

gtttanaaaa cttgtttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca	60
tgattctctg aggttaaact tgggtttcaa atgttatttt tacttgtatt ttgcttttgg	120
t	121

<210> 135

<211> 350
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 135

acttanaaacc	atgcctagca	catcagaatc	cctcaaagaa	catcagtata	atcctataacc	60
atancaagtg	gtgactgggt	aagcgtgcga	caaagggtcag	ctggcacatt	acttgtgtgc	120
aaacttgata	cttttgttct	aagtaggaac	tagtatacag	tncctaggan	tggtagtcca	180
gggtgcccc	caactcctgc	agccgctcct	ctgtgccagn	ccctgnaagg	aactttcgct	240
ccacctcaat	caagccctgg	gccatgctac	ctgcaattgg	ctgaacaaac	gtttgtgtgag	300
ttcccaagga	tgcaaagcct	ggtgctcaac	tcctggggcg	tcaactcagt		350

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136

tgtaccgtga	agacgacaga	agttgcatgg	cagggacagg	gcagggccga	ggccagggtt	60
gctgtgattg	tatccgaata	ntcctcgtga	gaaaagataa	tgagatgacg	tgagcagcct	120
gcagacttgt	gtctgccttc	aanaagccag	acaggaaggc	cctgcctgcc	ttggctctga	180
cctggcggcc	agccagccag	ccacaggtgg	gcttcttcct	tttgtggtga	caacnccaag	240
aaaactgcag	aggcccaggg	tcaggtgtna	gtgggtangt	gaccataaaa	caccaggtgc	300
tcccaggaa	ccgggcaaag	gccatcccca	cctacagcca	gcatgcccac	tggcgtgatg	360
ggtgcagang	gatgaagcag	ccagntgttc	tgctgtggt			399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(165)
 <223> n = A,T,C or G

<400> 137

actggtgtgg	tngggggtga	tgctggtggt	anaagttgan	gtgacttcan	gatggtgtgt	60
ggaggaagtg	tgtgaacgta	gggatgtaga	ngttttggcc	gtgctaaatg	agcttcggga	120
ttggctggtc	ccactggtgg	tcactgtcat	tggtgggggt	cctgt		165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 138

```

actcactgga atgccacatt cacaacagaa tcagaggctct gtgaaaacat taatggctcc      60
ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac      120
tgctgggcag tctcccatgc cttccacagt gaaagggtct gagaaaaatc acatccaatg      180
tcatgtgttt ccagccacac caaaagggtgc ttgggggtgga gggctggggg catananggt      240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa      300
aaaaactgat gccttttttt tttttttttg taaaattc                                338

```

```

<210> 139
<211> 382
<212> DNA
<213> Homo sapien

```

```

<400> 139
gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa      60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga      120
attcaaacag acctcgctcat tcttggtgtg agcctgggtcg gctcaccgcc tatcatctgc      180
atttgcccta ctcagggtgct accggactct ggcccctgat gtctgtagtt tcacaggatg      240
cctttattgt cttctacacc ccacagggcc cctacttctc tcggatgtgt ttttaataat      300
gtcagctatg tgcccacatc tccttcatgc cctccctccc tttctacca ctgctgagtg      360
gcctggaact tgtttaaagt gt                                382

```

```

<210> 140
<211> 200
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(200)
<223> n = A,T,C or G

```

```

<400> 140
acccaaanctt ctttctgttg tgtnngattt tactataggg gtttngcttn ttctaaanat      60
acttttcatt taacancttt tgtaagtgt caggctgcac ttgctccat anaattattg      120
ttttcacatt tcaacttgta tgtgtttgtc tottanagca ttggtgaaat cacatatattt      180
atattcagca taaaggagaa                                200

```

```

<210> 141
<211> 335
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(335)
<223> n = A,T,C or G

```

```

<400> 141
actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggttg      60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttgtt      120
atgcatgtag agaaccacaa ctaatttatt aaacaggata gaaacaggct gtctgggtga      180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg      240
ttttctacc agttcagaga tnggttaatg actanttcca atggggaaaa agcaagatgg      300
attcacaac caagtaattt taaacaaaga cactt                                335

```

```

<210> 142
<211> 459
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

<222> (1)...(459)

<223> n = A,T,C or G

<400> 142

accagggttaa	tattgccaca	tatatccttt	ccaattgcg	gctaaacaga	cgtgtattta	60
gggttggtta	aagacaaccc	agcttaatat	caagagaaat	tgtgacctt	catggagtat	120
ctgatggaga	aaacactgag	ttttgacaaa	tcttatttta	ttcagatagc	agtctgatca	180
cacatgggtcc	aacaacactc	aaataataaa	tcaaataatna	tcagatgtta	aagattggtc	240
ttcaaacatc	atagccaatg	atgccccgct	tgcctataat	ctctccgaca	taaaaccaca	300
tcaacacctc	agtggccacc	aaaccattca	gcacagcttc	cttaactgtg	agctgtttga	360
agctaccagt	ctgagcacta	ttgactatnt	ttttcanget	ctgaatagct	ctagggatct	420
cagcangggg	gggaggaacc	agctcaacct	tggcgctant			459

<210> 143

<211> 140

<212> DNA

<213> Homo sapien

<400> 143

acatttcctt	ccaccaagtc	aggactcctg	gcttctgtgg	gagttcttat	cacctgaggg	60
aaatccaaac	agtctctcct	agaaaggaat	agtgtcacca	acccacacca	tctccctgag	120
accatccgac	ttccctgtgt					140

<210> 144

<211> 164

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(164)

<223> n = A,T,C or G

<400> 144

acttcagtaa	caacatacaa	taacaacatt	aagtgtatat	tgccatcttt	gtcattttct	60
atctatacca	ctctcccttc	tgaaaacaan	aatcactanc	caatcactta	tacaaatttg	120
aggcaattaa	tccatatttg	ttttcaataa	ggaaaaaaag	atgt		164

<210> 145

<211> 303

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 145

acgtagacca	tccaactttg	tatttgtaat	ggcaaacatc	cagnagcaat	tcctaaacaa	60
actggagggt	atttatacc	aattatcca	ttcattaaca	tgccctcctc	ctcaggctat	120
gcaggacagc	tatcataagt	cggcccaggc	atccagatac	taccatttgt	ataaacttca	180
gtaggggagt	ccatccaagt	gacaggtcta	atcaaaggag	gaaatggaac	ataagcccag	240
tagtaaaatn	ttgcttagct	gaaacagcca	caaaagactt	accgccgtgg	tgattaccat	300
caa						303

<210> 146

<211> 327

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146

actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac	60
actggcctgg agtgactcat tgctctgggt ggttgagaga gctcccttgc caacaggcct	120
ccaagtcagg gctgggattt gtttcccttc cacattctag caacaatatg ctggccactt	180
cctgaacagg gagggaggga ggagccagca tggaacaagc tgccacttgc taaagtagcc	240
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg	300
taggggtgag ctgtgtgact ctatggt	327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147

acattgtttt tttgagataa agcattgana gagctctcct taacgtgaca caatggaagg	60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt	120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt	173

<210> 148
 <211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 148

acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc tttctatcct	60
atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact	120
gccctactac ctgctgcaat aatcacattc ccttctgtgc ctgaccctga agccattggg	180
gtggctcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac	240
nccancccac ctcaccgacc ccattcctctt acacagctac ctccttgctc tctaacccca	300
tagattatnt ccaaattcag tcaattaagt tactattaac actctaccgg acatgtccag	360
caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat	420
ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atggtgg	477

<210> 149
 <211> 207
 <212> DNA
 <213> Homo sapien

<400> 149

acagttgtat tataatatca agaaataaac ttgcaatgag agcattttaag agggaagaac	60
taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct	120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca	180
tttcaggcag agggaacagc agtgaaa	207

<210> 150
 <211> 111
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(111)
 <223> n = A,T,C or G

<400> 150
 accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60
 cacttaaattg tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151
 <211> 196
 <212> DNA
 <213> Homo sapien

<400> 151
 agcgcggcag gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac 60
 agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat 120
 ggataccaac cggaaaaccc ctatcccga cagccactg tggteccacac tgtctacgag 180
 gtgcacccgg ctcaagt 196

<210> 152
 <211> 132
 <212> DNA
 <213> Homo sapien

<400> 152
 acagcacttt cacatgtaag aaggagagaaa ttcttaaatg taggagaaaag ataacagaaac 60
 cttcccccctt tcatctagtgt gtggaaacct gatgctttat gttgacagga atagaaccag 120
 gagggagttt gt 132

<210> 153
 <211> 285
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(285)
 <223> n = A,T,C or G

<400> 153
 acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag 60
 cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctacagcagga 120
 gcacatcaat aaagtccaaa gtcttggaact tggccttggc ttggaggaag tcatcaacac 180
 cctggctagt gaggtgacgg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca 240
 gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt 285

<210> 154
 <211> 333
 <212> DNA
 <213> Homo sapien

<400> 154
 accacagtcc tgttgggcca gggcttcagt accctttctg tgaaaagcca tattatcacc 60
 accccaaatt ttcccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac 120
 cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg 180
 attggcacag gagtcgaagg tgttcagctc ccctcctccg tggaaacgaga ctctgatttg 240
 agtttcacaa attctcgggc cacctcgta ttgctcctct gaaataaaat ccggagaatg 300
 gtcaggcctg tctcatccat atggatcttc cgg 333

<210> 155

<211> 308
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(308)
 <223> n = A,T,C or G

<400> 155
 actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg 60
 gaaagtgcct tgggaactgt aaagtgccta acacatgac gatgattttt gttataatat 120
 ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagccccc 180
 atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggt 240
 gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcatgctg 300
 gccctggt 308

<210> 156
 <211> 295
 <212> DNA
 <213> Homo sapien

<400> 156
 accttgctcg gtgcttgga catattagga actcaaaata tgagatgata acagtgccta 60
 ttattgatta ctgagagAAC tgtagacat ttagttgaag attttctaca caggaactga 120
 gaataggaga ttatgtttgg cctcatatt ctctcctatc ctcttgctt cattctatgt 180
 ctaatatatt ctcaatcaa taaggttagc ataatcagga aatcgaccaa ataccaatat 240
 aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat 295

<210> 157
 <211> 126
 <212> DNA
 <213> Homo sapien

<400> 157
 acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct 60
 gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120
 cttagt 126

<210> 158
 <211> 442
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(442)
 <223> n = A,T,C or G

<400> 158
 acccactggt cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
 aanccagcag gctgcccta gtcagtcctt ccttcagag aaaaagagat ttgagaaagt 120
 gcctgggtaa ttcaccatta atttctccc ccaaactctc tgagtcttcc cttaatat 180
 ctggtggttc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240
 natgtttgta gccttgata cttagccctt cccacgcaca aacggagtgg cagagtgggt 300
 ccaaccctgt tttcccagtc cagtagaca gattcacagt gcggaattct ggaagctgga 360
 nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420
 tgttcattct ctgatgtcct gt 442

<210> 159
 <211> 498
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccaggt	aacgttggtg	tttccgttga	gcctgaactg	atgggtgacg	ttgtagggtc	60
tccaacaaga	actgagggtg	cagagcgggt	agggagaggt	gctgttccag	ttgcacctgg	120
gctgctgtgg	actgttggtg	attcctcact	acggcccaag	gttgtggaac	tggcanaaag	180
gtgtgttgtt	gganttgagc	tcgggcgggt	gtggtagggt	gtgggctctt	caacaggggc	240
tgctgtgggt	ccgggangtg	aanagtgttg	gtcacttgag	cttggccagc	tctggaaaag	300
antanattct	tcctgaaggc	cagcgcttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccagtg	ctgctgtggg	tgggtgtana	tcctccacaa	agcctgaagt	tatggtgtcn	420
tcaggtaana	atgtgggttc	agtgtccctg	ggcngctgtg	gaaggttgta	nattgtcacc	480
aagggaataa	gctgtggt					498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

acctgcatcc	agcttccctg	ccaaactcac	aaggagacat	caacctctag	acagggaaac	60
agcttcagga	tacttccagg	agacagagcc	accagcagca	aaacaaatat	tcccatgcct	120
ggagcatggc	atagaggaag	ctganaaatg	tggggtctga	ggaagccatt	tgagtctggc	180
cactagacat	ctcatcagcc	acttgtgtga	agagatgccc	catgaccca	gatgcctctc	240
ccacccttac	ctccatctca	cacacttgag	ctttccactc	tgtataattc	taacatcctg	300
gagaaaaatg	gcagtttgac	cgaacctgtt	cacaacggta	gaggctgatt	tctaacgaaa	360
cttgtagaat	gaagcctgga					380

<210> 161

<211> 114

<212> DNA

<213> Homo sapien

<400> 161

actccacatc	ccctctgagc	aggcggttgt	cgttcaaggt	gtatttgccc	ttgcctgtca	60
cactgtccac	tggcccctta	tccacttggt	gcttaatccc	tcgaaagagc	atgt	114

<210> 162

<211> 177

<212> DNA

<213> Homo sapien

<400> 162

actttctgaa	tcgaatcaaa	tgatacttag	tgtagtttta	atatcctcat	atatatcaaa	60
gttttactac	tctgataatt	ttgtaaacca	ggtaaccaga	acatccagtc	atacagcttt	120
tggtgatata	taacttggca	ataacccagt	ctggtgatata	ataaaactac	tcactgt	177

<210> 163

<211> 137

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(137)
 <223> n = A,T,C or G

<400> 163

catttataca	gacaggcgtg	aagacattca	cgacaaaaac	gcgaaattct	atcccgtgac	60
canagaaggc	agctacggct	actcctacat	cctggcgtgg	gtggccttcg	cctgcacctt	120
catcagcggc	atgatgt					137

<210> 164
 <211> 469
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(469)
 <223> n = A,T,C or G

<400> 164

cttatcacia	tgaatgttct	cctgggcagc	gttgatgatct	ttgccacott	cgtgacttta	60
tgcaatgcat	catgctatct	cataccta	gagggagttc	caggagattc	aaccaggaaa	120
tgcatggatc	tcaaaggaaa	caaacaccca	ataaaactcg	agtggcagac	tgacaactgt	180
gagacatgca	cttgctacga	aacagaaatt	tcatgttgca	cccttgtttc	tacacctgtg	240
ggttatgaca	aagacaactg	caaagaatc	ttcaagaagg	aggactgcaa	gtatatcgtg	300
gtggagaaga	aggacccaaa	aaagacctgt	tctgtcagtg	aatggataat	ctaattgtct	360
tctagtaggc	acagggctcc	caggccaggc	ctcattctcc	tctggcctct	aatagtcaat	420
gattgtgtag	ccatgcctat	cagtaaaaaag	atntttgagc	aaacacttt		469

<210> 165
 <211> 195
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(195)
 <223> n = A,T,C or G

<400> 165

acagtttttt	atanatatcg	acattgccgg	cacttggtgtt	cagtttcata	aagctgggtg	60
atccgctgtc	atccactatt	ccttggttag	agtaaaaaatt	attcttatag	cccatgtccc	120
tgcaggccgc	ccgccgtag	ttctcgttcc	agtcgtcttg	gcacacaggg	tgccaggact	180
tcctctgaga	tgagt					195

<210> 166
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 166

acatcttagt	agtgtggcac	atcagggggc	catcagggtc	acagtcactc	atagcctcgc	60
cgaggtcgga	gtccacacca	ccggtgtagg	tgtgtcfaat	cttgggcttg	gcgcccacct	120
ttggagaagg	gatatgctgc	acacacatgt	ccacaaagcc	tgtgaactcg	ccaaagaatt	180
tttgacagacc	agcctgagca	aggggcggat	gttcagcttc	agctcctcct	tcgtcagggtg	240
gatgccaacc	tcgtctangg	tccgtgggaa	gctgggtgtc	acntcaccta	caacctgggc	300
gangatctta	taaagaggct	ccnagataaa	ctccacgaaa	cttctctggg	agctgctagt	360

nggggccttt ttggtgaact ttc

383

<210> 167
<211> 247
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(247)
<223> n = A,T,C or G

<400> 167
acagagccag accttgGCCA taaatgaanc agagattaag actaaacccc aagtcganat 60
tgagacagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120
tatanccata cacagagcca actctcaggg caaggcniatg gttggggcag anccagagac 180
tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac 240
tganctc 247

<210> 168
<211> 273
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(273)
<223> n = A,T,C or G

<400> 168
acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60
aatccctcan ccttggttctt cactactgtc tatactgana gtgtcatgtt tccacaaagg 120
gctgacacct gagcctgnat tttcactcat ccttgagaag ccctttccag taggggtggc 180
aattcccaac ttccttgcca caagcttccc aggccttctc ccctggaaaa ctccagcttg 240
agtcccatgat acactcatgg gctgccctgg gca 273

<210> 169
<211> 431
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 169
acagccttgg cttcccaaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60
agctcagacc aggggtcaaa gatgtgacat caacagtttc tggtttcaga acaggttcta 120
ctactgtcaa atgaccccc atacttcctc aaaggctgtg gtaagttttg cacaggtgag 180
ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240
cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctg gcaccagctc 300
acgcacatca ctgacaaccg ggatggaaaa agaantgcca actttcatac atccaactgg 360
aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc 420
tcgaacactg a 431

<210> 170
<211> 266
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(266)
 <223> n = A,T,C or G

<400> 170

acctgtgggc	tgggctgtta	tgctgtgcc	ggctgtgaa	agggagtcca	gaggtggagc	60
tcaaggagct	ctgcaggcat	tttgccaanc	ctctccanag	canagggagc	aacctacact	120
ccccgctaga	aagacaccag	attggagtcc	tgggaggggg	agttgggggtg	ggcatttgat	180
gtatacttgt	cacctgaatg	aangagccag	agaggaanga	gacgaanatg	anattggcct	240
tcaaagctag	gggtctggca	ggtgga				266

<210> 171
 <211> 1248
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1248)
 <223> n = A,T,C or G

<400> 171

ggcagccaaa	tcataaacgg	cgaggactgc	agcccgcact	cgagccctg	gcaggcggca	60
ctggtcatgg	aaaacgaatt	gttctgctcg	ggcgtcctgg	tgcatccgca	gtgggtgctg	120
tcagccgcac	actgtttcca	gaagtgagtg	cagagctcct	acaccatcgg	gctgggcctg	180
cacagtcttg	aggccgacca	agagccaggg	agccagatgg	tggaggccag	cctctccgta	240
cggcacccag	agtacaacag	acccttgctc	gctaaccgacc	tcatgctcat	caagttggac	300
gaatccgtgt	ccgagtctga	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaact	cttgccctgt	ttctggctgg	ggtctgctgg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcgggtggg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	accccagcat	gttctgcgcc	ggcggagggc	aagaccagaa	ggactcctgc	540
aacggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgaggggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccagggtgtct	acaccaacct	ctgcaaattc	660
actgagtggg	tagagaaaac	cgtccaggcc	agtttaactct	ggggactggg	aaccatgaa	720
attgaccccc	aaatacatcc	tgcggaagga	attcaggaat	atctgttccc	agcccctcct	780
ccctcaggcc	caggagtcca	ggccccagc	ccctcctccc	tcaaaccaag	ggtacagatc	840
cccagcccct	cctccctcag	acccaggagt	ccagaccccc	cagcccctcc	tcctcagac	900
ccaggagtcc	agcccctcct	ccctcagacc	caggagtcca	gacccccag	cccctcctcc	960
ctcagaccca	gggggtccagg	cccccaaccc	ctcctccctc	agactcagag	gtccaagccc	1020
ccaaccntc	attccccaga	cccagaggtc	cagggtcccag	cccctcntcc	ctcagaccca	1080
gcggtccaat	gccacctaga	ctntccctgt	acacagtgcc	cccttggtggc	acgttgaccc	1140
aaccttacca	gttggttttt	catttttngt	ccctttcccc	tagatccaga	aataaagttt	1200
aagagaagng	caaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaa		1248

<210> 172
 <211> 159
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(159)
 <223> Xaa = Any Amino Acid

<400> 172

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1				5				10					15		
Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
			20					25					30		
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
			35				40					45			
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly

50	55	60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu		
65	70	75
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe		80
	85	90
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser		95
	100	105
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe		110
	115	120
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn		125
	130	135
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		140
145	150	155

<210> 173
 <211> 1265
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1265)
 <223> n = A,T,C or G

<400> 173

ggcagcccg	actcgcagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgttctgc	60
tcgggcgctc	tggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggctc	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gacccttgct	cgctaacgac	240
ctcatgctca	tcaagttgga	cgaatccgtg	tccgagtctg	acaccatccg	gagcatcagc	300
attgcttcgc	agtgccttac	cgcggggaac	tcttgccctg	tttctggctg	gggtctgctg	360
gcgaacgggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggtcctc	tgcccagtcg	420
cgggggctga	cccagagctc	tgcgtcccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcggg	ggtgtctgag	gaggtctgca	gtaagctcta	tgaccctgctg	taccacccca	540
gcatgttctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacggg	gactctgggg	600
ggcccctgat	ctgcaacggg	tacttgccag	gccttgtgtc	tttcggaaaa	gcccctgtgtg	660
gccaaagtgg	cggtgccagg	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tgggaaccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcctccctca	ggcccaggag	840
tccaggcccc	cagcccctcc	tcctccaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagaccag	gagtcagac	ccccagccc	ctcctccctc	agaccagga	gtccaggccc	960
tcctcctca	gacccaggag	tccagacccc	ccagcccctc	ctccctcaga	cccagggtt	1020
gaggccccca	acccctcctc	cttcagagtc	agaggtccaa	gcccccaacc	cctcgttccc	1080
cagacccaga	ggttnnaggc	ccagcccctc	ttcctcaga	cccagnggtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcccccttg	tgganagttg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

<210> 174
 <211> 1459
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1459)
 <223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagttag	tgcagagctc	ctacaccatc	gggctgggcc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagttgg	180

acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgccta	240
ccgcgggaa	ctcttgctc	gtttctggct	gggtctgct	ggcgaacgg	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	accagagct	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgacccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
caggggaagg	tggaagaagg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgagggcggt	780
gacctccacc	caatagaaaa	tectcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tggtgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttgttcaag	ggtcaactgt	1080
gtaccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aatcaagac	tctacaaaag	ggctgggcag	ggtgggtcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgctgt	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagaggtt	1380
gaagtgagtt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

<210> 175
 <211> 1167
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1167)
 <223> n = A,T,C or G

<400> 175						
gcgcagccct	ggcaggcggc	actggtcatg	gaaaacgaat	tggtctgctc	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccaga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagttagagc	aatccgtgtc	cgagtctgac	accatccgga	gcatacagcat	tgcttcgcag	300
tgccctaccg	cggggaactc	ttgcctcgtg	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcaactg	cgtgaacgtg	tgggtggtgt	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccc	gcggagggca	agaccagaag	480
gactcctgca	acggtgactc	tgggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaatcca	ctgagtggat	agagaaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccca	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gcccctcctc	cctcaggccc	aggagtccag	gccccagcc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagccctc	ctccctcaga	cccaggagtc	cagaccccc	agccctcnt	840
ccntcagacc	caggagtcca	gcccctcctc	cntcagacgc	aggagtccag	acccccagc	900
ccntcntccg	tcagaccag	gggtgcaggc	ccccaacccc	tcntccntca	gagtcagagg	960
tccaagcccc	caaccctcgt	ttccccagac	ccagaggtnc	aggtcccagc	ccctcctccc	1020
tcagacccag	cggtccaatg	ccacctagan	tnccctgtga	cacagtgcc	ccttgtggca	1080
ngttgaccca	accttaccag	ttggtttttc	attttttgtc	cctttccct	agatccagaa	1140
ataaagtnta	agagaagcgc	aaaaaaa				1167

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT

<222> (1)...(205)

<223> Xaa = Any Amino Acid

<400> 176

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Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20      25      30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35      40      45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
      50      55      60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
      65      70      75      80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
      85      90      95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
      100      105      110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
      115      120      125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
      130      135      140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
      145      150      155      160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
      165      170      175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
      180      185      190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
      195      200      205

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<210> 177

<211> 1119

<212> DNA

<213> Homo sapien

<400> 177

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gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc      60
gtcctgggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctccacacc      120
atcgggctgg ccctgcacag tcttgaggcc gaccaagagc cagggagcca gatgggtgag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300
tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctgggggtct gctggcgaa      360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc      420
caaccctggc agggttgtac catttcggca acttccagt caaggacgtc ctgctgcac      480
ctcactgggt gctcactact gctcactgca tcacccgaa cactgtgat aactagccag      540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt      600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc      660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc      720
tgacctacag aggtgaggga tcatatagct ctccaaggat gctgggtact ccctcacaaa      780
ttcatttctc ctgtttagt gaaagggtgc ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtacac cagggcaggc ctagcatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg      1020
gagggtgagg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc      1080
ttaataaaca gaagctgtga tgtaaaaaa aaaaaaaaaa      1119

```

<210> 178

<211> 164

<212> PRT

<213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

<400> 178
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1 5 10 15
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35 40 45
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50 55 60
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
 100 105 110
 Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
 115 120 125
 Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
 130 135 140
 Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
 145 150 155 160
 Pro Gly Thr Leu

<210> 179
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 179
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgcc cgcgcgggg gatgcgaggc tcggagcacc ctgcccggc tgtgattgct 120
 gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga 180
 aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa 240
 aaaaaaaaaa 250

<210> 180
 <211> 202
 <212> DNA
 <213> Homo sapien

<400> 180
 actagtccag tgtggtggaa ttccattgtg ttggggcccaa cacaatggct acctttaaca 60
 tcaccagac cccgccctg cccgtgcccc acgtgctgc taacgacagt atgatgctta 120
 ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc 180
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181
 <211> 558
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(558)
 <223> n = A,T,C or G

<400> 181
 tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg 60
 aatgttttagg cagtgtcagt aatttcytcg taatgattct gttattactt tcctnattct 120
 ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa 180
 ggtagtgtga tagtataagt atctaagtc agatgaaagt gtgttatata tatccattca 240
 aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac 300
 ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa 360
 attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw 420
 ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt 480
 aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc 540
 caaaaaaaaa aaaaaaaaa 558

<210> 182
 <211> 479
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 182
 acagggwttk grggatgcta agsccccrga rwtygtttga tccaaccctg gcttwttttc 60
 agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmg gcacccctgg 120
 cstcacacag astcccgagt agctgggact acaggcacac agtcactgaa gcaggccctg 180
 ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca 240
 ctaagggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca 300
 tactmttcta agtcctcttc cagcctcact kkgagtccctm cytggggggtt gataggaant 360
 ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcatara 420
 awtgstgara aaattaaaat gttctgggty mactttaaaa aaaaaaaaaa aaaaaaaaaa 479

<210> 183
 <211> 384
 <212> DNA
 <213> Homo sapien

<400> 183
 aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactgggtgcc 60
 agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgct 120
 ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt 180
 gccagcacca gtggcagctc tgggtgcctgt ggtttctcct acaagtgaga ttttagatat 240
 tgtaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca 300
 cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt 360
 gccatttcaa aaaaaaaaaa aaaa 384

<210> 184
 <211> 496
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(496)
 <223> n = A,T,C or G

<400> 184
 accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatcac ctcaacgagc 60
 agggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgtctag 120
 cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga 180
 aacgcttcaa ggtgctcatg acccagcaac cgcgccctgt cctctgaggg tcccttaaac 240
 tgatgtcttt tctgccacct gttacccctc ggagactccg taaccaaact cttcgagactg 300

tgagccctga	tgcctttttg	ccagccatac	tctttggcat	ccagtctctc	gtggcgattg	360
attatgcttg	tgtgaggcaa	tcattggtgg	atcacccata	aagggaacac	atttgacttt	420
tttttctcat	attttaaatt	actacmagaw	tattwmagaw	waaatgawtt	gaaaaactst	480
taaaaaaaaa	aaaaaa					496

<210> 185
 <211> 384
 <212> DNA
 <213> Homo sapien

<400> 185	
gctggtagcc	tatggcgkkg
cccacggagg	ggctcctgag
gccacggrac	agtgaacttc
caagtatcyt	gcgcsgcgtc
ttctaccgtc	cctacctgca
gatcttcggg	cagattcccc
aggaggacat	ggacgtggcc
ctcatggagc	acagcaactg
ytcgctggag	cccggcttct
gggcacaccc	tcttggggcc
caggcgggca	cctgcgtctc
ccagtatgcc	aactggctgg
tggtgctgct	cctcgtcatc
ttcctgctcg	tggccaacat
cctgctggtc	aacttgctca
ttgccatgtt	cagttacaca
ttcggcaaag	tacagggcaa
cagcgatctc	tactgggaag
gcgcagcgtt	accgcctcat
cggg	

<210> 186
 <211> 577
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(577)
 <223> n = A,T,C or G

<400> 186	
gagttagctc	ctccacaacc
ttgatgaggt	cgtctgcagt
ggcctctcgc	ttcataccgc
tnccatcgtc	atactgtagg
tttgccacca	cytcctggca
tcttggggcg	gcntaatatt
ccaggaaact	ctcaatcaag
tcaccgtcga	tgaacctgt
gggctgggtc	tgtcttccgc
tcggtgtgaa	aggatctccc
agaaggagtg	ctcgatcttc
cccacacttt	tgatgacttt
attgagtcga	ttctgcatgt
ccagcaggag	gttgtaaccag
ctctctgaca	gtgaggtcac
cagccctatc	atgccgttga
mcgtgccgaa	garcaccgag
ccttgtgtgg	gggkkggaag
ctcaccaga	ttctgcatta
ccagagagcc	gtggcaaaag
acattgacaa	actcgcccag
gtggaaaaag	amcamctcct
ggargtgctn	gccgctcctc
gtcmgttgg	ggcagcgctw
tccttttgac	acacaaaaca
gttaaaggca	ttttcagccc
ccagaaantt	gtcatcatcc
aagatntcgc	acagcactna
tccagttggg	attaaat

<210> 187
 <211> 534
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(534)
 <223> n = A,T,C or G

<400> 187	
aacatcttcc	tgtataatgc
tgtgtaatat	cgatccgatn
ttgtctgstg	agaatycatw
actkggaaaa	gmaacattaa
agcctggaca	ctgggtattaa
aattcacaa	atgcaacact
ttaaacagt	tgtcaatctg
ctcccyynac	tttgtcatca
ccagtctggg	aakaagggtg
tgccctattc	acacctgtta
aaagggcgct	aagcattttt
gattcaacat	cttttttttt
gacacaagtc	cgaaaaaagc
aaaagtaaac	agttatyaat
ttgtagcca	attcactttc
ttcatgggac	agagccatyt
gatttaaaaa	gcaaattgca
taatattgag	cttygggagc
tgatatttga	gcggaagagt
agcctttcta	cttcaccaga
cacaactccc	tttcatattg
ggatgttnac	naaagtwatg
tctctwacag	atgggatgct
tttgtggcaa	ttctgttctg
aggatctccc	agtttattta
ccacttgcac	aagaaggcgt
tttcttctc	aggc

<210> 188
 <211> 761
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(761)
 <223> n = A,T,C or G

<400> 188
 agaaaccagt atctctnaaa acaacctctc ataccttggt gacctaatTT tgtgtgcgtg 60
 tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg 120
 cctcttttgt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180
 ttgtcttctg tgtaaattggt actagagaaa acacctatnt tatgagtcaa tctagttngt 240
 tttattcgac atgaaggaaa ttccagatn acaacactna caaactctcc ctkgackarg 300
 ggggacaaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa 360
 acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt 420
 gcaaaaaaca tgtacngact tcccgttgag taatgccaag ttgttttttt tatnataaaa 480
 cttgcccttc attacatggt tnaaagtggg gtggtggggc aaaatattga aatgatggaa 540
 ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac 600
 atgcttaatt cacaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta 660
 tttttctgtn ttccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac 720
 gaaaataata acattgaaga aaaaananaaa aaanaaaaaa a 761

<210> 189
 <211> 482
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 189
 tttttttttt ttggccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca 60
 caccggggct atnagaagca agaagggaagg agggagggca cagccccttg ctgagcaaca 120
 aagccgctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc 180
 aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggangtgt gcataagaag 240
 tgataggcac aggccaccg gtacagacc ctcggtcct gacaggtnga ttctgaccag 300
 gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc ttctctttc 360
 aaatttggt ngtcatngaa ngggcanttt tccaantng gctnggtctt ggtacncttg 420
 gttcggccca gctccncgtc caaaaantat tcaccnct ccnaattgt tgcnngnccc 480
 cc 482

<210> 190
 <211> 471
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(471)
 <223> n = A,T,C or G

<400> 190
 tttttttttt ttttaaaaca gtttttcaca aaaaaattta ttagaagaat agtggttttg 60
 aaaactctcg catccagtga gaactacat acaccacatt acagctngga atgtntcca 120
 aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag 180
 cgcttttgac atacaatgca caaaaaaaa aggggggggg gaccacatgg attaaaattt 240
 taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt 300

```

tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantncteta 360
ctacatcnac cttgatcatt gccaggaach aaaagttnaa ancaacnngt acaaaaaanaa 420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c 471

```

```

<210> 191
<211> 402
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

```

```

<400> 191
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct 60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa 120
attcttcacc agtcacatct tctaggacct ttttgattc agttagtata agctcttcca 180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaaagg aattyaattg 240
ctcgttctct aacaatgtcc tctccttgaa gtatttggtc gaacaaccca cctaaagtcc 300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc 360
aagatgcata tgtctgcaaa agttgcgtta gtatatctgc ca 402

```

```

<210> 192
<211> 601
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(601)
<223> n = A,T,C or G

```

```

<400> 192
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60
ggtctacccc acatgggagc agcatgccgt agntatataa ggatcattccc tgagtcagac 120
atgcytyttt gaytaccgtg tgccaagtgc tggatgattct yaacacacyt ccatcccggt 180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc 240
acgagacact tgaaagggtgt aacaaagcga ytcttgcaat gctttttgtc cctccggcac 300
cagttgtcaa tactaaccgc ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360
tacatctcct gacagtactg aagaacttct tcttttggtt caaaagcarg tcttggtgcc 420
tggttgatca gggtccattt tcccagtcyg aatgttcaca tggcatattt wacttcccac 480
aaaacattgc gatttgagge tcagcaacag caaatcctgt tccggcattg gctgcaagag 540
cctcgatgta gccggccagc gccaaaggcag gcgccgtgag ccccaccagc agcagaagca 600
g 601

```

```

<210> 193
<211> 608
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(608)
<223> n = A,T,C or G

```

```

<400> 193
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60
gggtccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgactctytt 120
cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tctgtggcttg gggtkgacgg 180
tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccagc tgtgcgggac 240
ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggccagc ggccttgccc 300

```

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctccggcctcg 360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgcgcgcctc 420
caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtrattggcgt 480
ctgcagtggt tttgtcgatg ttctccaggc acaggctggc cagctgcggt tcatcgaaga 540
gtcgcgcctg cgtgagcagc atgaaggcgt tgcggtctcg cagttcttct tcaggaactc 600
cacgcaat 608

```

```

<210> 194
<211> 392
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

```

```

<400> 194
gaacggctgg accttgctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt 60
ccagtcgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc 120
tccgcctcaa tgcagaacca gtatggggag cactgtgttt agagttaaga gtgaacactg 180
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac 240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagttagtg attctgtatt 300
taaagaaaat attactgta catatactgc ttgcaatttc tgtatttatt gktnctstgg 360
aaataaatat agttattaaa ggtgtcant cc 392

```

```

<210> 195
<211> 502
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(502)
<223> n = A,T,C or G

```

```

<400> 195
ccsttkgagg ggtkaggkyc cagttccga gtggaagaaa caggccagga gaagtgcgtg 60
ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc 120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc 180
aagggaaggc ccattccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc 240
ccccagagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca 300
caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact 360
gscscacacc caccagagc acgccaccgg ccatggggar tgtgctcaag gartcgcngg 420
gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt 480
gctnanaaaa aaaaanaaaa aa 502

```

```

<210> 196
<211> 665
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(665)
<223> n = A,T,C or G

```

```

<400> 196
ggttacttgg ttctattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga 180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac 240

```

aagtatgatg	aaaagcaawa	gatatatatt	cttttattat	gttaaattat	gattgccatt	300
attaatcggc	aaaatgtgga	gtgtatgttc	ttttcacagt	aatatatgcc	ttttgtaact	360
tcacttggtt	atthttattgt	aaatgartta	caaaattctt	aatttaagar	aatgggtatgt	420
watatttatt	tcattaattt	ctttcctkgt	ttacgtwaat	tttgaaaaga	wtgcatgatt	480
tcttgacaga	aatcgatctt	gatgctgtgg	aagtagtgtg	accacatcc	ctatgagttt	540
ttcttagaat	gtataaagg	tgtagcccat	cnaacttcaa	agaaaaaat	gaccacatac	600
tttgcaatca	ggctgaaatg	tggcatgctn	ttctaattcc	aactttataa	actagcaaan	660
aagtg						665

<210> 197
 <211> 492
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(492)
 <223> n = A,T,C or G

ttttnttttt	ttttttttgc	aggaaggatt	ccattttattg	tggatgcatt	ttcacaatat	60
atgtttattg	gagcgatcca	ttatcagtga	aaagtatcaa	gtgtttataa	natttttagg	120
aaggcagatt	cacagaacat	gctngtcngc	ttgcagtttt	acctcgtana	gatnacagag	180
aattatagtc	naaccagtaa	acnaggaatt	tacttttcaa	aagattaaat	ccaaactgaa	240
caaaatttcta	ccctgaaact	tactccatcc	aaatattgga	ataanagtca	gcagtgtac	300
attctcttct	gaactttaga	ttttctagaa	aaatattgaa	tagtgatcag	gaagagctct	360
tgttcaaaag	tacaacnaag	caatgttccc	ttaccatagg	ccttaattca	aactttgatc	420
catttcactc	ccatcacggg	agtcaatgct	acctgggaca	cttgattttt	gttcatnctg	480
ancntggctt	aa					492

<210> 198
 <211> 478
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(478)
 <223> n = A,T,C or G

ttntttttgn	atttcantct	gtannaanta	ttttcattat	gtttattana	aaaatatnaa	60
tgtntccacn	acaaatcatn	ttacntnagt	aagaggccan	ctacattgta	caacatacac	120
tgagtatatt	ttgaaaagga	caagtttaaa	gtanacncat	attgccganc	atanacatt	180
tatacatggc	ttgattgata	tttagcacag	canaaactga	gtgagttacc	agaaanaaat	240
natatatgtc	aatcngattt	aagatacaaa	acagatccta	tggtacatan	catcntgtag	300
gagttgtggc	tttatgttta	ctgaaagtca	atgcagttcc	tgtacaaaga	gatggccgta	360
agcattctag	tacctctact	ccatgggtta	gaatcgtaca	cttatgttta	catatgtnta	420
gggtaagaat	tgtgttaagt	naanttatgg	agaggtccan	gagaaaaatt	tgatncaa	478

<210> 199
 <211> 482
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(482)
 <223> n = A,T,C or G

agtgacttgt	cctccaacaa	aaccccttga	tcaagtttgt	ggcaactgaca	atcagaccta	60
------------	------------	------------	------------	-------------	------------	----

tgctagttcc	tgatcatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaatctatt	cctacttgta	cggactttga	180
agtgattcag	tttcctctac	ggatgagaga	ctggctcaag	aatatcctca	tgacgcttta	240
tgaagccnac	tctgaacacg	ctgggttatct	nagatgagaa	ncagagaaat	aaagtcnaga	300
aaatttacct	ggangaaaag	aggctttngg	ctggggacca	tcccattgaa	ccttctctta	360
anggacttta	agaanaaaact	accacatgtn	tgtngtatcc	tggtgccngg	ccgtttantg	420
aacntngacn	ncacccttnt	ggaatanant	cttgacngcn	tcttgaactt	gctcctctgc	480
ga						482

<210> 200
 <211> 270
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(270)
 <223> n = A,T,C or G

<400> 200						
cggccgcaag	tgcaactcca	gctggggccg	tgccgacgaa	gattctgcca	gcagttggtc	60
cgactgcgac	gacggcgccg	gcgacagtcg	caggtgcagc	gcgggcgcct	gggtccttgc	120
aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtcccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggt	gaangcggga	ggcctcgggg	agcccctcgg	gaagggcggc	240
ccgagagata	cgcaggtgca	ggtggccgcc				270

<210> 201
 <211> 419
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(419)
 <223> n = A,T,C or G

<400> 201						
tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttatatttga	60
gctagcaagg	taacagggtg	gggcatgggt	acatgttcag	gtcaacttcc	tttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaancgaagc	anaantaaca	180
tgagtggtgt	gcaccctccc	tgtagaacct	ggttacnaaa	gcttggggca	gttcacctgg	240
tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatata	ttttagagag	300
tccactgtnt	ctggagggag	attagggttt	cttgccaana	tccaancaaa	atccacttga	360
aaaagttgga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cgggtggcca	419

<210> 202
 <211> 509
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(509)
 <223> n = A,T,C or G

<400> 202						
ttnttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tggcacttaa	tccattttta	tttcaaaatg	tctacaaant	ttnaatncnc	cattatacng	120
gtnattttnc	aaaatctaaa	nnttattcaa	atntnagcca	aantccttac	ncaaatnnaa	180
tacncncaaa	aatcaaaaat	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa	240
aatatatacg	gctgggtgtt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnaa	300
ggaactaaaa	taaaaaaaaa	cactnccgca	aagggttaaag	ggaacaacaa	attcntttta	360

caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng 420
 ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca 480
 caatgnaat nccncncnc tggactagt 509

<210> 203

<211> 583

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 203

tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttatttttact 60
 tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
 taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
 gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
 atttttcttg tctttaaaat tatctaattc ttccattttt tccctattcc aagtcaattt 300
 gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa 360
 agggaaaaa ggaagagana atggcacaca aaacaaacat tttatattca tatttctacc 420
 tacgttaata aaatagcatt ttgtgaagcc agctcaaaag aaggcttaga tccttttatg 480
 tccattttag tcaactaaacg atatcnaaag tgccagaatg caaaagggtt gtgaacattt 540
 attcaaaagc taatataaga tatttcacat actcatcttt ctg 583

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 204

ttttttttnt tttttttttt ttttttntc ttcttttttt ttganaatga ggatcgagtt 60
 ttctactctc tagatagggc atgaagaaaa ctcatctttc cagcttttaa ataacaatca 120
 aatctcttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc 180
 tgaaggaaaat ctgttcattc ttctcattca tatagttata tcaagtacta ccttgcatat 240
 tgagagggtt ttcttctcta ttacacata tatttccatg tgaatttgta tcaaaccttt 300
 attttcatgc aaactagaaa ataattgntt cttttgcata agagaagaga acaatatnag 360
 cattacaaaa ctgctcaaat tgtttgtaa gnttatccat tataattagt tnggcaggag 420
 ctaatacaaa tcacatttac ngacnagcaa taataaaaact gaagtaccag ttaaatatcc 480
 aaaataatta aagggaacatt tttagcctgg gtataattag ctaattcact ttacaagcat 540
 ttattnagaa tgaattcaca tgttattatt ccntagccca acacaatgg 589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

ttttnttttt ttttttcagt aataatcaga acaatattta tttttatatt taaaattcat 60
 agaaaagtgc cttacattta ataaaagttt gtttctcaaa gtgatcagag gaattagata 120
 tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaatat 180

```

ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt 240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat 300
atgggggtgac actggtaaac caacacattc tgaaggatac attacttagt gatagattct 360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt 420
aaggggcnaga ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatngg 480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga 540
aaccc 545

```

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<210> 206
<211> 487
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

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```

<400> 206
tttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt 60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna 120
caatttataa atgtaagggtg ccattattga gtanatatat tctccaaga gtggatgtgt 180
cccttctccc accaactaat gaancagcaa cattagttaa attttattag tagatnatac 240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag 300
ttggtnagaa tgcatacanca atctnacaat caacagcaag atgaagctag gcntgggctt 360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cggtggcaag 420
aactcttcga accgcttcct caaaggcnagc tgccacattt gtggcntctn ttgcacttgt 480
ttcaaaa 487

```

```

<210> 207
<211> 332
<212> DNA
<213> Homo sapien

```

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<220>
<221> misc_feature
<222> (1)...(332)
<223> n = A,T,C or G

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```

<400> 207
tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
tacaatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggtcactact 120
gcatttatag gaccttctgg tggttctgct gttacnttg aantctgaca atccttgana 180
atctttgcat gcagaggagg taaaaggat tggattttca cagaggaana acacagcgca 240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
aaaagaaggc agcctaggcc ctggggagcc ca 332

```

```

<210> 208
<211> 524
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(524)
<223> n = A,T,C or G

```

```

<400> 208
agggcggtgt ggggagggcg ttactgtttt gtctcagtaa caataaatac aaaaagactg 60
gttgtgttcc ggccccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
tttaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180
tccgcggtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaatact 240

```

tttggcagaa tacttnttga aacttgcaga tgataactaa gatccaagat atttcccaaa	300
gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagttcca ttacaagtc	360
atgagcccag aactgacat caaactaagc ccacttagac tcctcaccac cagtctgtcc	420
tgtcatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatccaa	480
aaaccattac ctgatccact tccggtaatg caccaccttg gtga	524

<210> 209

<211> 159

<212> DNA

<213> Homo sapien

<400> 209

gggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg	60
tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca	120
caaaggactc tcgacccaaa ctgccccaga ccctctcca	159

<210> 210

<211> 256

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(256)

<223> n = A,T,C or G

<400> 210

actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc	60
actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta	120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgaggagat	180
ttgcagggtg naaatggan ggctggtttg ttanatgaac agggacatag gaggtaggca	240
ccaggtgct aatca	256

<210> 211

<211> 264

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(264)

<223> n = A,T,C or G

<400> 211

acattgtttt ttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg	60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt	120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga	180
ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga	240
aaaaaaggag caaatgagaa gcct	264

<210> 212

<211> 328

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(328)

<223> n = A,T,C or G

<400> 212

acccaaaaat ccaatgctga atatttggct tcattattcc canattcttt gattgtcaaa	60
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ggattttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180
ttnaatttca ttcccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240
ccccacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300
tttttttttc ctttattcct ttgtcaga 328

```

```

<210> 213
<211> 250
<212> DNA
<213> Homo sapien

```

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<220>
<221> misc_feature
<222> (1)...(250)
<223> n = A,T,C or G

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```

<400> 213
acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt 60
taaagcattg ctcaactgaag ggatagaagt gactgccagg agggaaaagta agccaaggct 120
cattatgccca aagganatat acatttcaat tctccaaact tcttctcat tccaagagtt 180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct 240
tctcatcggt 250

```

```

<210> 214
<211> 444
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(444)
<223> n = A,T,C or G

```

```

<400> 214
accagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag 60
gatttaagt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg 120
tttatatatg cagcaacaat attcaagcgc gacaacaggg tattgaactt gcccggcagg 180
tgaatttcat tcccattgac ttgggaccc tatcatcagc canagagatt gaaaatttac 240
ccctacgact ctttactctc tggagagggc cagtgggtgt agctataagc ttggccacat 300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag 360
agtgaacttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt 420
actttgctct ccctaataata cctc 444

```

```

<210> 215
<211> 366
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = A,T,C or G

```

```

<400> 215
acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt 60
taaagcattg ctcaactgaag ggatagaagt gactgccagg agggaaaagta agccaaggct 120
cattatgccca aagganatat acatttcaat tctccaaact tcttctcat tccaagagtt 180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct 240
tctcatcggt aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa 300
tccaagctgt tttctacact gtaaccagggt ttccaaccaa ggtggaaatc tcttatactt 360
ggtgcc 366

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<210> 216
 <211> 260
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(260)
 <223> n = A,T,C or G

<400> 216
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctntnc atttttttat 120
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttingctgga aaatttaaaa 180
 atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
 aattcttctt tcctctctt 260

<210> 217
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 217
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
 tcttgccat aattttctat tttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
 ggcatctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
 atatccttca tgcttgtaaa gt 262

<210> 218
 <211> 205
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(205)
 <223> n = A,T,C or G

<400> 218
 accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120
 aggctcccc agttctactg acctttgtcc ttangntna ngctccagggt tgctaggaaa 180
 anaaatcagc agacacaggt gtaaa 205

<210> 219
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 219
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
 <211> 93
 <212> DNA

<213> Homo sapien

<400> 220

actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60
aaataagcat ttagtgctca gtccctactg agt 93

<210> 221

<211> 167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(167)

<223> n = A,T,C or G

<400> 221

actangtgca ggtgcgcaca aatatttgct gatattccct tcatcttgga ttccatgagg 60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120
ccccactac cttccctgac gctcccccana aatcacccaa cctctgt 167

<210> 222

<211> 351

<212> DNA

<213> Homo sapien

<400> 222

agggcggtgt gcgaggggct gtactgacct cattagtagg aggatgcatt ctggcacccc 60
gttcttcacc tgtcccccac tccttaaaag gccatactgc ataaagtcaa caacagataa 120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240
taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt 300
ctcgtatcaa aacaatagat tggtaaagggt ggtattattg tattgataag t 351

<210> 223

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 223

aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60
tggttaattat ggtcaattta atwrtttkt ggggcatttc cttacattgt cttgacaaga 120
ttaaaatgtc tgtgccaaaa ttttgatttt tatttgagga cttcttatca aaagtaatgc 180
tgccaaagga agtctaagga attagtagtg ttcccmctac ttgtttggag tgtgctattc 240
taaaagattt tgatttcctg gaatgacaat tatattttta ctttggtggg ggaaanagtt 300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg 360
accattaagc tatatgttta aaa 383

<210> 224

<211> 320

<212> DNA

<213> Homo sapien

<400> 224

cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
aaaagtttgt gacattgtag tagggagtgt gtaccctta ctcccatca aaaaaaaat 120
ggatacatgg ttaaaggata raagggcaat attttatcat atgttctaaa agagaaggaa 180

gagaaaatac tactttctcr	aaatggaagc	ccttaaaggt	gctttgatac	tgaaggacac	240
aaatgtggcc gtccatcctc	ctttaragtt	gcatgacttg	gacacggtaa	ctggttgagc	300
tttaractcm gcattgtgac					320

<210> 225

<211> 1214

<212> DNA

<213> Homo sapien

<400> 225

gaggactgca gcccgcactc	gcagccctgg	caggcgccac	tggatcatgga	aaacgaattg	60
ttctgctcgg gcgtcctggt	gcattccgag	tgggtgctgt	cagccgcaca	ctggtttccag	120
aactcctaca ccacgaggct	gggcctgcac	agtcttgagg	ccgaccaaga	gccaggagac	180
cagatggtgg aggccagcct	ctccgtacgg	caccagaggt	acaacagacc	cttgctcgct	240
aacgacctca tgctcatcaa	gttggacgaa	tccgtgtccg	agtctgacac	catccggagc	300
atcagcattg ctctgcagtg	ccctaccgag	gggaactctt	gcctcgtttc	tggctggggg	360
ctgctggcga acggcagaa	gctaccgtg	ctgcagtgcg	tgaacgtgtc	ggtgggtgtc	420
gaggagggtc gcagtaagct	ctatgaccg	ctgtaccacc	ccagcatgtt	ctgcgcgggc	480
ggagggcaag accagaagga	ctcctgcaac	ggtgactctg	gggggcccct	gatctgcaac	540
gggtacttgc agggccttgt	gtctttcgga	aaagccccgt	gtggccaagt	tggcgtgcca	600
ggtgtctaca ccaacctctg	ca'aattcact	gagtggatag	agaaaaccgt	ccaggccagt	660
taactctggg gactgggaac	ccatgaaatt	gacccccaaa	tacatcctgc	ggaaggaatt	720
caggaataat tgttcccagc	ccctcctccc	tcaggcccag	gagtcagagc	ccccagcccc	780
tcctccctca aaccaagggt	acagatcccc	agccccctct	ccctcagacc	caggagtcca	840
gacccccag cccctcctcc	ctcagaccga	ggagtccagc	ccctcctccc	tcagaccag	900
gagtcagac cccccagccc	ctcctccctc	agaccagggg	gtccaggccc	ccaacccttc	960
ctccctcaga ctcagaggtc	caagccccca	accctcctt	ccccagacc	agaggtccag	1020
gtcccagccc ctccctccctc	agaccagcgg	gtccaatgcc	acctagactc	tcctgtaca	1080
cagtgcctcc ttgtggcag	ttgacccaac	cttaccagtt	ggtttttcat	ttttgtccc	1140
tttcccttag atccagaaat	aaagtctaag	agaagcgcaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa aaaa					1214

<210> 226

<211> 119

<212> DNA

<213> Homo sapien

<400> 226

accagtatg tgcagggaga	cggaacccca	tgtgacagcc	cactccacca	gggttcccaa	60
agaacctggc ccagtcataa	tcattcatcc	tgacagtggc	aataatcacg	ataaccagt	119

<210> 227

<211> 818

<212> DNA

<213> Homo sapien

<400> 227

acaattcata gggacgacca	atgaggacag	ggaatgaacc	cggtctctcc	ccagccctga	60
ttttgtctac atatggggtc	ccttttcatt	ctttgcaaaa	acactggggt	ttctgagaac	120
acggacgggt cttagcaca	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttctc ctctggagga	aaggtggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca cgctcgccct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc ttccaatcag	ccaattctga	gaacccccat	ctaacttctc	actggaaaag	360
agggcctcct caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaggggt caccctcagc	agagaagccg	agagcttaac	tctggctggt	tccagagaca	480
acctgctggc tgtcttgga	tgcgccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcatgagagg	600
gacaggctct gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcagc	660
aaagccattc ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct aggttttcag	cctagatggg	agtcgtgt			818

<210> 228
 <211> 744
 <212> DNA
 <213> Homo sapien

<400> 228
 actggagaca ctgttgaact tgatcaagac ccagaccacc ccaggtctcc ttogtgggat 60
 gtcacatgacgt ttgacataacc tttggaacga gcctcctcct tggaagatgg aagaccgtgt 120
 tcgtggccga cctggcctct cctggcctgt ttcttaagat gcggagtcac atttcaatgg 180
 taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga 240
 tgctcgggtgc acattggggt gctttgggat aaaagattta tgagccaact attctctggc 300
 accagattct aggccagttt gttccactga agcttttccc acagcagtc accctctgcag 360
 gctggcagct gaatggcttg ccggtggctc tgtggcaaga tcacactgag atcgatgggt 420
 gagaaggcta ggatgcttgt ctagtgttct tagctgtcac gttggctcct tccaggttgg 480
 ccagacgggtg ttggccactc ccttctaaaa cacaggcgcc ctccgtgtga cagtgacccg 540
 ccgtggtatg ccttggccca ttccagcagt cccagttatg catttcaagt ttggggtttg 600
 ttcttttctg taatgttctt ctgtgtgtgc agctgtcttc atttctggg ctaagcagca 660
 ttgggagatg tggaccagag atccactcct taagaaccag tggcgaaaga cactttcttt 720
 cttcactctg aagtagctgg tgggt 744

<210> 229
 <211> 300
 <212> DNA
 <213> Homo sapien

<400> 229
 cgagtctggg ttttgtctat aaagtgtgat cctcctttt ctcatccaaa tcatgtgaac 60
 cattacacat cgaaataaaa gaaaggtggc agacttgccc aacgccaggc tgacatgtgc 120
 tgcagggttg ttgttttta attattattg ttagaaacgt caccacagc ccctgttaat 180
 ttgtatgtga cagccaactc tgagaaggtc ctatttttcc acctgcagag gatccagtct 240
 cactaggctc ctccctgccc tcacactgga gtctccgcca gtgtgggtgc ccactgacat 300

<210> 230
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 230
 cagcagaaca aatacaaata tgaagagtgc aaagatctca taaaatctat gctgaggaat 60
 gagcgacagt tcaaggagga gaagcttgca gagcagctca agcaagctga ggagctcagg 120
 caatataaag tcctggttca cactcaggaa cgagagctga cccagttaag ggagaagttg 180
 cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggecct cctcactccg 240
 gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac 300
 g

<210> 231
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 231
 gcaagcacgc tggcaaactc ctgtcaggtc agctccagag aagccattag tcatttttagc 60
 caggaaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120
 ggcaacacgg gacttctcat cagggaagtgg gatgtagatg agctgatcaa gacggccagg 180
 tctgaggatg gcaggatcaa tgatgtcagg ccggttgga ccgccaatga tgaacacatt 240
 tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300
 c 301

<210> 232
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 232

agtaggtatt	tcgtgagaag	ttcaacacca	aaactggaac	atagttctcc	ttcaagtgtt	60
ggcgacagcg	gggcttcctg	attctggaat	ataactttgt	gtaaattaac	agccacctat	120
agaagagtcc	atctgctgtg	aaggagagac	agagaactct	gggttcgctc	gtcctgtcca	180
cgtgctgtac	caagtgtctg	tgccagcctg	ttacctgttc	tactgaaaa	tctggctaata	240
gctcttgtgt	atcacttctg	attctgacaa	tcaatcaatc	aatggcctag	agcactgact	300
g						301

<210> 233

<211> 301

<212> DNA

<213> Homo sapien

<400> 233

atgactgact	tcccagtaag	gctctctaag	gggtaagtag	gaggatccac	aggatttgag	60
atgctaaggc	cccagagatc	gtttgatcca	accctcttat	tttcagaggg	gaaaatgggg	120
cctagaagtt	acagagcatc	tagctgggtc	gctggcacc	ctggcctcac	acagactccc	180
gagtagctgg	gactacaggc	acacagtcac	tgaagcaggc	cctgttagca	attctatgcg	240
tacaaattaa	catgagatga	gtagagactt	tattgagaaa	gcaagagaaa	atcctatcaa	300
c						301

<210> 234

<211> 301

<212> DNA

<213> Homo sapien

<400> 234

aggctctaca	catcgagact	catccatgat	tgatatgaat	ttaaaaatta	caagcaaaga	60
cattttattc	atcatgatgc	tttcttttgt	ttcttctttt	cgttttcttc	tttttctttt	120
tcaattttcag	caacatactt	ctcaatttct	tcaggattta	aaatcttgag	ggattgatct	180
cgctcatga	cagcaagttc	aatgtttttg	ccacctgact	gaaccacttc	caggagtgcc	240
ttgatcacca	gcttaatggt	cagatcatct	gcttcaatgg	cttcgtcagt	atagttcttc	300
t						301

<210> 235

<211> 283

<212> DNA

<213> Homo sapien

<400> 235

tggggctgtg	catcaggcgg	gtttgagaaa	tattcaattc	tcagcagaag	ccagaatttg	60
aattccctca	tcttttaggg	aatcatttac	caggtttgga	gaggattcag	acagctcagg	120
tgctttcact	aatgtctctg	aacttctgtc	cctctttgtt	catggatagt	ccaataaata	180
atgttatctt	tgaactgatg	ctcataggag	agaatataag	aactctgagt	gatatcaaca	240
ttagggattc	aaagaaatat	tagattttaag	ctcacactgg	tca		283

<210> 236

<211> 301

<212> DNA

<213> Homo sapien

<400> 236

aggctctcca	ccaactgcct	gaagcacggg	taaaattggg	aagaagtata	gtgcagcata	60
aatactttta	aatcgatcag	atttccttaa	cccacatgca	atcttcttca	ccagaagagg	120
tcggagcagc	atcattaata	ccaagcagaa	tgcgtaatag	ataaatacaa	tggtatatag	180
tgggtagacg	gcttcatgag	tacagtgtac	tgtggatcgc	taatctggac	ttgggttgta	240
aagcatcggt	taccagtcag	aaagcatcaa	tactcgacat	gaacgaatat	aaagaacacc	300
a						301

<210> 237

<211> 301

<212> DNA

<213> Homo sapien

<400> 237

cagtggtagt	ggtgggtggac	gtggcggttg	tcgtgggtgcc	ttttttggtg	cccgtcacaa	60
actcaatttt	tgttcgctcc	tttttgccct	tttccaattt	gtccatctca	attttctggg	120
ccttggctaa	tgccatcatag	taggagtcct	cagaccagcc	atggggatca	aacatatcct	180
ttgggtagtt	ggtgccaagc	tcgtcaatgg	cacagaatgg	atcagcttct	cgtaaatacta	240
gggttccgaa	attctttctt	cctttggata	atgtagttca	tatccattcc	ctcctttatc	300
t						301

<210> 238

<211> 301

<212> DNA

<213> Homo sapien

<400> 238

gggcagggttt	tttttttttt	ttttttgatg	gtgcagaccc	ttgctttatt	tgtctgactt	60
gttcacagtt	cagccccctg	ctcagaaaac	caacgggcca	gctaaggaga	ggaggaggca	120
ccttgagact	tccggagtcg	aggctctcca	gggttcccca	gcccataaat	cattttctgc	180
acccctgcc	tgggaagcag	ctccctgggg	ggtgggaatg	ggtgactaga	agggatttca	240
gtgtgggacc	cagggtctgt	tcttcacagt	aggaggtgga	agggatgact	aattttcttta	300
t						301

<210> 239

<211> 239

<212> DNA

<213> Homo sapien

<400> 239

ataagcagct	agggaattct	ttatttagta	atgtcctaac	ataaaagtgc	acataactgc	60
ttctgtcaaa	ccatgatact	gagctttgtg	acaaccacga	aataactaag	agaaggcaaa	120
cataatacct	tagagatcaa	gaaacattta	cacagttcaa	ctgtttaaaa	atagctcaac	180
attcagccag	tgagtagagt	gtgaatgcc	gcatacacag	tatacaggtc	cttcaggga	239

<210> 240

<211> 300

<212> DNA

<213> Homo sapien

<400> 240

ggtcctaagt	aagcagcagc	ttccacattt	taacgcaggt	ttacgggtgat	actgtccttt	60
gggatctgcc	ctccagtgga	accttttaag	gaagaagtgg	gcccagctca	agttccacat	120
gctgggtgag	ccagatgact	tctgttcctt	ggtcactttc	ttcaatgggg	cgaatggggg	180
ctgccagggt	tttaaaatca	tgcttcatct	tgaagcacac	ggtcacttca	ccctcctcac	240
gctgtgggtg	tactttgatg	aaaataccca	ccttggttgc	ctttctgaag	ctataatgac	300

<210> 241

<211> 301

<212> DNA

<213> Homo sapien

<400> 241

gaggctctggt	gctgaggtct	ctgggctagg	aagaggagtt	ctgtggagct	ggaagccaga	60
cctcttttga	ggaaactcca	gcagctatgt	tggtgtctct	gagggaatgc	aacaaggctg	120
ctcctccatg	tattggaaaa	ctgcaaaactg	gactcaactg	gaaggaagtg	ctgctgccag	180
tggaagaac	cagcctgagg	tgacagaaac	ggaagcaaac	aggaacagcc	agtcttttct	240
tcctcctcct	gtcatacggg	ctctctcaag	catcctttgt	tgtcaggggc	ctaaaaggga	300
g						301

<210> 242

<211> 301

<212> DNA

<213> Homo sapien

<400> 242

ccgaggtcct	gggatgcaac	caatcactct	gtttcacgtg	acttttatca	ccatacaatt	60
tgtggcattt	cctcattttc	tacattgtag	aatcaagagt	gtaaataaat	gtatatcgat	120
gtcttcaaga	atatatcatt	cctttttcac	tagaacccat	tcaaaatata	agtcaagaat	180
cttaatatca	acaaatatat	caagcaaact	ggaaggcaga	ataactacca	taatttagta	240
taagtacca	aagttttata	aatcaaaagc	cctaatagata	accattttta	gaattcaatc	300
a						301

<210> 243

<211> 301

<212> DNA

<213> Homo sapien

<400> 243

aggttaagtc	cagtttgaag	ctcaaaagat	ctggatgag	cataggctca	tcgacgacat	60
ggtggcccaa	gctatgaaat	cagagggagg	cttcatctgg	gcctgtaaaa	actatgatgg	120
tgacgtgcag	tcggactctg	tggcccaagg	gtatggctct	ctcgcatga	tgaccagcgt	180
gctggtttgt	ccagatggca	agacagtaga	agcagaggct	gcccacggga	ctgtaacccg	240
tcaactaccg	atgttccaga	aaggacagga	gacgtccacc	aatcccattg	cttccatttt	300
t						301

<210> 244

<211> 300

<212> DNA

<213> Homo sapien

<400> 244

gctggtttgc	aagaatgaaa	tgaatgattc	tacagctagg	acttaacctt	gaaatggaaa	60
gtcatgcaat	cccatttgca	ggatctgtct	gtgcacatgc	ctctgtagag	agcagcattc	120
ccagggacct	tggaaacagt	tgacactgta	aggtgcttgc	tccccaagac	acatocctaaa	180
aggtgttgta	atggtgaaaa	cgtcttcctt	ctttattgcc	ccttcttatt	tatgtgaaca	240
actggttgte	ttttgtgtat	cttttttaaa	ctgtaaaagt	caattgtgaa	aatgaatatc	300

<210> 245

<211> 301

<212> DNA

<213> Homo sapien

<400> 245

gtctgagtat	ttaaaatggt	attgaaatta	tccccaacca	atgttagaaa	agaaagaggt	60
tatatactta	gataaaaaat	gaggtgaatt	actatccatt	gaaatcatgc	tcttagaatt	120
aaggccagga	gatattgtca	ttaatgtara	cttcaggaca	ctagagtata	gcagccctat	180
gttttcaaag	agcagagatg	caattaaata	ttgttttagca	tcaaaaaggc	cactcaatac	240
agctaataaa	atgaaagacc	taatttctaa	agcaattcct	tataatttac	aaagttttaa	300
g						301

<210> 246

<211> 301

<212> DNA

<213> Homo sapien

<400> 246

ggtctgtcct	acaatgcctg	cttcttgaaa	gaagtcggca	ctttctagaa	tagctaaata	60
acctgggctt	attttaaaga	actatttgta	gctcagattg	gttttcctat	ggctaaaata	120
atgtgttctt	gtgaaaatta	aataaaaacag	ttaattcaaa	gccttgatat	atgttaccac	180
taacaatcat	actaaatata	ttttgaagta	caaagtttga	catgctctaa	agtgacaacc	240
caaagtgtgc	ttacaaaaca	cgttcctaac	aaggtatgct	ttacactacc	aatgcagaaa	300
c						301

<210> 247
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 247
 aggtcctttg gcagggctca tggatcagag ctcaaactgg agggaaaggc atttcgggta 60
 gcctaagagg gcgactggcg gcagcacaac caaggaaggc aaggttggtt cccccacgct 120
 gtgtcctgtg ttcaggtgcg acacacaatc ctcatgggaa caggatcacc catgcgctgc 180
 ccttgatgat caaggttggg gcttaagtgg attaaggag gcaagttctg ggttccttgc 240
 cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta 300
 a 301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttagaatt 120
 acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
 gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240
 ctaatgagac tggatttttg tttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
 c 301

<210> 249
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 249
 gtccagagga agcacctggg gctgaactag gcttgccctg ctgtgaactt gcaattggag 60
 ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccggcc 120
 ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc 180
 catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
 actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
 a 301

<210> 250
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 250
 ggtctgtgac aaggacttgc aggtgtggg aggcaagtga cccttaacac tacacttctc 60
 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
 cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac 180
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
 caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
 a 301

<210> 251
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 251
 gccgaggtcc tacatttggc ccagtttccc cctgcatcct ctccagggcc cctgcctcat 60
 agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120
 ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
 cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga 240

cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300
c 301

<210> 252
<211> 301
<212> DNA
<213> Homo sapien

<400> 252
gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttggtg catttcctca 60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata 120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa 180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt 240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc 300
a 301

<210> 253
<211> 301
<212> DNA
<213> Homo sapien

<400> 253
ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctcga ttctcgtacc 60
caactaaaaa aaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct 120
tggtctgatt gtttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg 180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt 240
tccatagtgc ccacagggtg ttctcacat tttctccata ggaaaatgct ttttcccaag 300
g 301

<210> 254
<211> 301
<212> DNA
<213> Homo sapien

<400> 254
cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg 60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc 120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa 180
gaaaaaaata agcttttga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc 240
acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc 300
t 301

<210> 255
<211> 302
<212> DNA
<213> Homo sapien

<400> 255
agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa 60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat 120
tggtattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180
aggaaaaagg actggagggt gaatctttat aaaaaacaag agtgattgag gcagattgta 240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac 300
aa 302

<210> 256
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

80

<222> (1)...(301)

<223> n = A,T,C or G

<400> 256

gttccagaaa	acattgaagg	tggtttoccca	aagtctaact	agggataccc	cctctagcct	60
aggaccctcc	tccccacacc	tcaatccacc	aaaccatcca	taatgcaccc	agataggccc	120
acccccaaaa	gcctggacac	cttgagcaca	cagttatgac	caggacagac	tcattctctat	180
aggcaaatag	ctgctggcaa	actggcatta	cctggtttgt	ggggatgggg	gggcaagtgt	240
gtggcctctc	ggcctggtta	gcaagaacat	tcagggtagg	cctaagttaa	tcgtgttagt	300
t						301

<210> 257

<211> 301

<212> DNA

<213> Homo sapien

<400> 257

gttgtggagg	aactctggct	tgctcattaa	gtcctactga	ttttcactat	cccctgaatt	60
tccccactta	tttttgtctt	tcactatcgc	aggccttaga	agaggtctac	ctgcctccag	120
tcttacctag	tccagtctac	cccctggagt	tagaatggcc	atcctgaagt	gaaaagtaat	180
gtcacattac	tcccttcagt	gatttcttgt	agaagtgcc	atccctgaat	gccaccaaga	240
tcttaattct	cacatcttta	atcttatctc	tttgactcct	ctttacaccg	gagaaggctc	300
c						301

<210> 258

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 258

cagcagtagt	agatgccgta	tgccagcacg	cccagcactc	ccaggatcag	caccagcacc	60
agggggcccag	ccaccaggcg	cagaagcaag	ataaacagta	ggctcaagac	cagagccacc	120
cccaggggcaa	caagaatcca	ataccaggac	tgggcaaaaat	cttcaaagat	cttaacactg	180
atgtctcggg	cattgaggct	gtcaataana	cgctgatccc	ctgctgtatg	gtgggtgcat	240
tgggtatccc	tgggagcgcc	ggtggagtaa	cgttggtcca	tggaaagcag	cgcccacaac	300
t						301

<210> 259

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 259

tcatatatgc	aaacaaatgc	agactangcc	tcaggcagag	actaaaggac	atctcttggg	60
gtgtcctgaa	gtgatttgga	cccctgaggg	cagacaccta	agtaggaatc	ccagtgggaa	120
gcaaagccat	aaggaagccc	aggattcctt	gtgatcagga	agtgggccag	gaaggctctg	180
tccagctcac	atctcatctg	catgcagcac	ggaccggatg	cgcccactgg	gtcttggctt	240
ccctcccatc	ttctcaagca	gtgtccttgt	tgagccattt	gcataccttg	ctccagggtg	300
c						301

<210> 260

<211> 301

<212> DNA

<213> Homo sapien

<400> 260

tttttttct	ccctaaggaa	aaagaaggaa	caagtctcat	aaaaccaa	aagcaatggt	60
aaggtgtctt	aacttgaaaa	agattaggag	tcactggttt	acaagttata	attgaatgaa	120
agaactgtaa	cagccacagt	tggccatttc	atgccaatgg	cagcaaaca	caggattaac	180
tagggcaaaa	taaataagtg	tgtggaagcc	ctgataagtg	cttaataaac	agactgattc	240
actgagacat	cagtacctgc	ccggggcgcc	gctcgagccg	aattctgcag	atatccatca	300
c						301

<210> 261

<211> 301

<212> DNA

<213> Homo sapien

<400> 261

aaatattcga	gcaaactctg	taactaatgt	gtctccataa	aaggctttga	actcagtga	60
tctgcttcca	tccacgattc	tagcaatgac	ctctcggaca	tcaaagctcc	tcttaaggtt	120
agcaccaact	attccataca	attcatcagc	aggaaataaa	ggctcttcag	aaggttcaat	180
ggtgacatcc	aatttcttct	gataatttag	attcctcaca	accttcctag	ttaagtgaag	240
ggcatgatga	tcacccaaag	cccagtggtc	acttactcca	gactttctgc	aatgaagatc	300
a						301

<210> 262

<211> 301

<212> DNA

<213> Homo sapien

<400> 262

gaggagagcc	tgttacagca	tttgtaagca	cagaatactc	caggagtatt	tgtaattgtc	60
tgtgagcttc	ttgccgcaag	tctctcagaa	atttaaaaag	atgcaaattc	ctgagtcacc	120
cctagacttc	ctaaaccaga	tcctctgggg	ctggaacctg	gcactctgca	tttgtaatga	180
gggctttctg	gtgcacacct	aattttgtgc	atctttgccc	taaactctgg	attagtgtcc	240
catcattacc	cccacattat	aatgggatag	attcagagca	gatactctcc	agcaaagaat	300
c						301

<210> 263

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 263

tttagcttgt	ggtaaagac	tcacaaaact	gattttaaaa	tcaagttaat	gtgaattttg	60
aaaattacta	cttaaatccta	attcacataa	acaatggcat	taaggtttga	cttgagttgg	120
ttcttagtat	tatttatggg	aaataggctc	ttaccacttg	caaataactg	gccacatcat	180
taatgactga	cttcccagta	aggctctcta	aggggtaagt	angaggatcc	acaggatttg	240
agatgctaag	gccccagaga	tcgtttgatc	caaccctctt	attttcagag	gggaaaatgg	300
g						301

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

aaagacgtta	aaccactcta	ctaccacttg	tggaactctc	aaagggtaaa	tgacaaaacc	60
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aatgaatgac tctaaaaaca atattttacat ttaatgggtt gtagacaata aaaaaacaag 120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaaag 180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240
acccttcata taaattcact atcttggcct gagggcactcc ataaaatgta tcacgtgcat 300
a 301

```

```

<210> 265
<211> 301
<212> DNA
<213> Homo sapien

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<400> 265
tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattcttct 60
cttcttctga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta 120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga 180
ttttcagttt gtcaacatgt tctctaaca cacttgccca tttctgtaaa gaatccaaag 240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300
c 301

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```

<210> 266
<211> 301
<212> DNA
<213> Homo sapien

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<400> 266
taccgtctgc ccttcctccc atccaggcca tctgcgaatc tacatgggtc ctcctattcg 60
acaccagatc actcttttct ctaccacag gcttgctatg agcaagagac acaacctcct 120
ctcttctgtg ttccagcttc ttttctgtt cttcccaccc ctttaagttct attcctgggg 180
atagagacac caatacccat aacctctctc ctaagcctcc ttataacca ggggtgcacag 240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg 300
a 301

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<210> 267
<211> 301
<212> DNA
<213> Homo sapien

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<400> 267
aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg 60
gtttctcagt ctgagtgcat ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc 120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaagc 180
ctcattctga ttctctcctc tcttttcttt caagtgggtc ttcctcacat cctctgttcc 240
aattegcctc agcttgtctg ctttagccct catttcacga agcttcttct ctttggcatc 300
t 301

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```

<210> 268
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 268
aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60
gatcttggga gagctgggtc ttctaaggag aaggagggaag gacagatgta actttggatc 120
tcgaagagga agtctaattg aagtaattag tcaacggtcc ttgttttagac tcttgggaata 180
tgctgggtgg ctacgtgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca 240
cttcccattg ttctactttc taccatcacc aattgtatat tatgtattct ttggagaact 300
a 301

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<210> 269
<211> 301
<212> DNA
<213> Homo sapien

```

<400> 269
 taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60
 aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120
 atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180
 cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240
 tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300
 t 301

<210> 270
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 270
 cattgaagag cttttgcgaa acatcagaac acaagtgcct ataaaattaa ttaagcctta 60
 cacaagaata catattcctt ttattttctaa ggagttaaac atagatgtag ctgatgtgga 120
 gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa 180
 ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240
 tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggcct aacagaaaac 300
 a 301

<210> 271
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 271
 aaaaggttct cataagatta acaattttaa taaatatttg atagaacatt ctttctcatt 60
 tttatagctc atcttttagg ttgatattca gttoatgctt ccttgctgt tcttgatcca 120
 gaattgcaat cacttcatca gctgtattc gctccaattc tctataaagt ggggtccaagg 180
 tgaaccacag agccacagca cactctttc ccttggtgac tgccttcacc ccatganggt 240
 tctctcctcc agatganaac tgatcatgag cccacatttt gggttttata gaagcagtca 300
 c 301

<210> 272
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 272
 taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc 60
 ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120
 tccaataatt cctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca 180
 gcatcttctc caacaaatat aaccttgagt ggcttctgt aatctatgtt ctttgttttc 240
 ctaaggactt ccattgcatc tcctacaata ttttctctac gcaccactag aattaagcag 300
 g 301

<210> 273
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 273

acatgtgtgt	atgtgtatct	ttgggaaaaa	aanaagacat	cttgtttayt	atTTTTTTgg	60
agagangctg	ggacatggat	aatcacwtaa	tttgctayta	tyactTTaat	ctgactygaa	120
gaaccgtcta	aaaataaaat	ttaccatgtc	dtatatcct	tatagtatgc	ttatttcacc	180
ttYtttctgt	ccagagagag	tatcagtgc	ananatttma	gggtgaamac	atgmattggt	240
gggacttnty	tttacngagm	accctgcccg	sgcgccctcg	makcngantt	ccgcsananc	300
t						301

<210> 274

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 274

cttatatact	ctttctcaga	ggcaaaagag	gagatgggta	atgtagacaa	ttctttgagg	60
aacagtaa	gattattaga	gagaanga	ggaccaagga	gacagaaatt	aacttgtaaa	120
tgattctctt	tggaatctga	atgagatcaa	gaggccagct	ttagcttggtg	gaaaagtcca	180
tctaggtatg	gttgcatctt	cgtcttcttt	tctgcagtag	ataatgaggt	aaccgaaggc	240
aattgtgctt	cttttgataa	gaagctttct	tggtcatatc	aggaaattcc	aganaaagtc	300
c						301

<210> 275

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 275

tcgggtgtcag	cagcacgtgg	cattgaacat	tgcaatgtgg	agcccaaacc	acagaaaatg	60
gggtgaaatt	ggccaacttt	ctattaactt	atggtggcaa	ttttgccacc	aacagtaagc	120
tggcccttct	aataaaagaa	aattgaaagg	tttctcacta	aacggaatta	agtagtggag	180
tcaagagact	cccaggcctc	agcgtacctg	cccggggcggc	cgctcgaagc	cgaattctgc	240
agatatccat	cacactggcg	gncgctcgan	catgcatcta	gaaggnccaa	ttcgccctat	300
a						301

<210> 276

<211> 301

<212> DNA

<213> Homo sapien

<400> 276

tgtagacata	ctcaataaat	aatgactgc	attgtgggtat	tattactata	ctgattatat	60
ttatcatgtg	acttctaatt	agaaaatgta	tccaaaagca	aaacagcaga	tatacaaaat	120
taaagagaca	gaagatagac	attaacagat	aaggcaactt	atacattgag	aatccaaatc	180
caatacattt	aaacatttgg	gaaatgaggg	ggacaaatgg	aagccagatc	aaatttgtgt	240
aaaactattc	agtatgtttc	ccttgcttca	tgtctgagaa	ggctctcctt	caatggggat	300
g						301

<210> 277

<211> 301

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 277
 tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaaag 60
 atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120
 gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccc aacctgctct 180
 caccatagtg gggagactaa agtggccacg gatttgctt anggtgacag tgcgttctga 240
 gttcncgtgc gattacatct gaccagtctc ctttttccga agtcctccg ttcaatcttg 300
 c 301

<210> 278
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgta 120
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacagggtt 240
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt accttccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaagggtg gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120
 tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
 gtttgatata gtttagggtt ggggttagat taagatctaa attacatcag gacaaagaga 240
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
 t 301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatc 60
 gccgagcaat ccaaactctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
 tgtgtagcac actgcgatta cagctaaata acccgtaatt gtgtgtcatg tttgcatttc 240
 tgacaagtga aacaggatct tacgatggag tttgtatga aaacaaagt gacgtacctc 300
 g 301

<210> 282
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 282
 caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
 tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
 agcgcagaag caaagcccag gcagaacat gctaacctta cagctcagcc tgcacagaag 180
 cgcagaagca aagcccagc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
 cagaagcaaa gccccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
 a 301

<210> 283
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 283
 atctgtatc ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60
 cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
 gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
 acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240
 ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
 g 301

<210> 284
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 284
 caggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60
 gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa 120
 gcagattagg tttttgacaa aacaaacagg ccaaaaagggg gctgacctgg agcagagcat 180
 ggtgagaggc aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt 240
 actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300
 a 301

<210> 285
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 285
 acatcaccat gatcgatcc cccacccatt atacgttgta tgtttacata aatactcttc 60
 aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120
 caggaaagca aatgctatct acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
 attaaatag tctgacttct ttgaggtca cagcactagg caaatgctat ttacgatctg 240
 caaagctgt ttgaagagtc aaagccccca tgtgaacacg atttctggac cctgtaacag 300
 t 301

<210> 286
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 286
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
 tgtatattat ttttgcccta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
 atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccaccca 180
 aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240
 gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt tttcccttg 300
 t 301

<210> 287
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 287
 tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
 cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120
 aaatgatttg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180
 ccgtggttat ctctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240
 gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300
 t 301

<210> 288
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 288
 gtacaccta ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
 agtcaatagg aagacaaatt ccagttccag ctcatctgga gtatctgcaa agctgcaaaa 120
 gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
 aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag 240
 tctgccttaa ttttgatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
 a 301

<210> 289
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 289
 ggtacactgt ttccatgtta tgtttctaca cattgctacc tcagtgtccc tggaaactta 60
 gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg 120
 ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180

cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggcggcgaan aagagaaaaga 240
 tgtgttttgt tttggactct ctgtgggcc ttccaatgct gtgggtttcc aaccagnnga 300
 a 301

<210> 290
 <211> 301
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 290
 aactgagct cttcttgata aatatacaga atgcttgcca tataacaagat tctatactac 60
 tgactgatct gttcatttct ctcacagctc ttaccccca aagcttttcc accctaagtg 120
 ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg 180
 gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc 240
 tgccctgaac aaaaacattt ctccatgtct catitttctc atgcctcaag taacagtgaag 300
 a 301

<210> 291
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 291
 caggtaccaa tttcttctat cctagaaaca tttcatttta tgttggtgaa acataacaac 60
 tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120
 tttactcttt tgtttatagg tgaatcacaa aatgtatttt tatgtattct gtagttcaat 180
 agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa 240
 acatgagctt cacttcccca ctaactaatt agcatctgtt atttcttaac cgtaatgcct 300
 a 301

<210> 292
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 292
 accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc 60
 tgtattaaat aatttttaag tttaaaagat aaaataccat catttttaaat gttgggtattc 120
 aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaaatgat ttgcnagatg 180
 ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc 240
 tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa 300
 a 301

<210> 293
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 293
 ggtaccaagt gctgggtgcca gcctgttacc tgttctcact gaaaagtctg gctaagtctc 60
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt 120
 aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180

gtgagaatTT tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
 g 301

<210> 294
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 294
 tgaccataa caatatacac tagctatctt tttaaactgtc catcattagc accaatgaag 60
 attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120
 tttaaactata gtcacaganc ttaaataatc acattgtttt ctatgtctac tgaaaataag 180
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
 cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt 300
 t 301

<210> 295
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 295
 gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttgtg aatccatctt gctttttccc cattgggaact agtcattaac ccatctctga 180
 actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggt. 240
 tctcagaacc atttcacca gacagcctgt ttctatcctg ttaataaat tagtttgggt 300
 tctct 305

<210> 296
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 296
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180
 ttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240
 tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300
 c 301

<210> 297
 <211> 300
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(300)
 <223> n = A,T,C or G

<400> 297
 actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60
 aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120
 acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180

tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgg 300

<210> 298
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (301)
<223> n = A,T,C or G

<400> 298
tatgggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgcccggctg 120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccaccct 180
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg 300
t 301

<210> 299
<211> 301
<212> DNA
<213> Homo sapien

<400> 299
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca ggtctctgc 60
tcaactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc 120
tgggattgca ggctcagcc accataccca gctaattttt ttgtattttt agtagagacg 180
gagtttgcgc atgttgcca gctggctca aactcctgac ctcaagcgac ctgcctgcct 240
cggcctccca aagtgtgga attataggca tgagtcaaca cgcccagcct aaagatatatt 300
t 301

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

<400> 300
attcagtttt atttgcctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
tatgtcccac acccactggg aaaggctccc acctggctac ttctctatc agctgggtca 120
gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta 180
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtottgttac 240
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccagcg catccccat 300
g 301

<210> 301
<211> 301
<212> DNA
<213> Homo sapien

<400> 301
ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120
gggaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaagacc 180
ctcagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
t 301

<210> 302
<211> 301

<212> DNA

<213> Homo sapien

<400> 302

```

aggtacacat ttagcttgtg gtaaatagact cacaaaaactg attttaaaat caagttaatg      60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aagggttgac      120
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg      180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca      240
caggatttga gatgctaagg cccagagat cgtttgatcc aacctctta ttttcagagg      300
g                                     301

```

<210> 303

<211> 301

<212> DNA

<213> Homo sapien

<400> 303

```

aggtaccaac tgtggaaata ggtagaggat ctttttttct ttccatatca actaagttgt      60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac      120
tggctaattg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc      180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc      240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac      300
c                                     301

```

<210> 304

<211> 301

<212> DNA

<213> Homo sapien

<400> 304

```

acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaatt      60
tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc      120
cttttttagtg tatcatatca ggaatcatct cacattgggt tgtgccatta ctgggtgcagt      180
gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga      240
ttttcccttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatataatct      300
c                                     301

```

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

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gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag      60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggag      120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggatttc tcatgcctag      180
aatattggtg gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggaacaaaa      240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag      300
a                                     301

```

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

Val Leu Gly Trp Val Ala Glu Leu

1

5

<210> 307
 <211> 637
 <212> DNA
 <213> Homo sapien

<400> 307

acaggggratg	aagggaaagg	gagaggatga	ggaagccccc	ctggggattt	ggtttggtcc	60
ttgtgatcag	gtggtctatg	gggcttatcc	ctacaaagaa	gaatccagaa	ataggggcac	120
attgaggaat	gatacttgag	cccaaagagc	attcaatcat	tgttttattt	gccttmtttt	180
cacaccattg	gtgagggagg	gattaccacc	ctggggttat	gaagatggtt	gaacacccca	240
cacatagcac	cggagatatg	agatcaacag	tttcttagcc	atagagattc	acagcccaga	300
gcaggaggac	gcttgccacac	catgcaggat	gacatggggg	atgcgctcgg	gattgggtgtg	360
aagaagcaag	gactgttaga	ggcaggcttt	atagtaacaa	gacggtgggg	caaactctga	420
tttccgtggg	ggaatgtcat	ggtcttgctt	tactaagttt	tgagactggc	aggtagtga	480
actcattagg	ctgagaacct	tgtggaatgc	acttgaccga	sctgatagag	gaagtagcca	540
ggtgggagcc	tttcccagtg	ggtgtggggac	atatctggca	agattttgtg	gcactcctgg	600
ttacagatac	tggggcagca	aataaaaactg	aatcttg			637

<210> 308
 <211> 647
 <212> DNA
 <213> Homo sapien

<220>

<221> misc feature

<222> (1) ... (647)

<223> n = A, T, C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
gnggcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccacccctct	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggttaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
cattttgtgt	gtggataaag	tcaggatgcc	cagggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccaatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	tttttctcct	gcttctgact	tgataaaaag	ggaccgt		647

<210> 309
 <211> 460
 <212> DNA
 <213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaataac	tcattcattt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctgggggtgt	ggagcgaacc	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttgtt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310
 <211> 539
 <212> DNA
 <213> Homo sapien

93

```

<400> 310
acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg      60
ctaaagggtt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt      120
taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa      180
gtcagacagt aagatttgtg ggaaatgggt tggtttgttg tatggtatgt attttagcaa      240
taatctttat ggcagagaaa gctaaaatcc ttttagcttg gtgaatgatc acttgctgaa      300
ttctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac      360
ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc acactgtgac      420
atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc      480
atattttcac cccacaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga      539

```

```

<210> 311
<211> 526
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(526)
<223> n = A,T,C or G

```

```

<400> 311
caaatttgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc      60
ttttgacggt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta      120
cattacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa      180
attaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg      240
ttttcaciaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa      300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc      360
tctctttaca gggagctcct gcagccccta cagaaatgag tggctgagat tcttgattgc      420
acagaagag cttctcatct aaacccttct cctttttagt atctgtgtat caagtataaa      480
agttctataa actgtagtnt acttatttta atcccaaaag cacagt      526

```

```

<210> 312
<211> 500
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

```

```

<400> 312
cctctctctc cccacccct gactctagag aactgggttt tctcccagta ctccagcaat      60
tcatttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct      120
ccatttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgct atgagtgtaa      180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg      240
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atccctctt      300
tgcatatgtc tagcagcttc agacatttgg ttaagaaccc atgggaaaaa aaaaaatcct      360
tgctaattgt gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct      420
ctgaacgtgt ggtaaagatt tttgtgttg aatataggag aaatcagttt gctgaaaagt      480
tagtottaat tatctattgg

```

```

<210> 313
<211> 718
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(718)

```

<223> n = A, T, C or G

<400> 313

ggagatttgt	gtggtttgca	gccgaggag	accaggaaga	tctgcatggt	gggaaggacc	60
tgatgataca	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtgcac	gtttttgcac	atttccagcc	cttttaaata	tccacacaca	caggaagcac	240
aaaaggaagc	acagagatcc	ctgggagaaa	tgcccggccg	ccatcttggg	tcacgatga	300
gcctcgccct	gtgcctgntc	ccgcttggtg	gggaaggaca	ttagaaaatg	aattgatgtg	360
ttccttaaag	gatggcagga	aaacagatcc	tgttgtggat	atattttga	acgggattac	420
agatttgaaa	tgaagtcaca	aagtgcagcat	taccaatgag	aggaaaacag	acgagaaaat	480
cttgatggtt	cacaagacat	gcaacaaaca	aaatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaatac	tgacttacgg	660
ttcttntggc	ccacattttc	atnatccacc	ccntcntttt	aannttantic	caaantgt	718

<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

gtttattttac	attacagaaa	aaacatcaag	acaatgtata	ctatttcaaa	tatatccata	60
cataatcaaa	tatagctgta	gtacatgttt	tcattgggtg	agattaccac	aaatgcaagg	120
caacatgtgt	agatctcttg	tcttattctt	ttgtctataa	tactgtattg	tgtagtccaa	180
gctctcggtg	gtccagccac	tgtgaaacat	gctcccttta	gattaacctc	gtggacgctc	240
ttgttgtatt	gctgaactgt	agtgcctgt	attttgcctc	tgtctgtgaa	ttctgttgc	300
tctggggcat	ttccttgtga	tgcagaggac	caccacacag	atgacagcaa	tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

taccacctcc	ccgctggcac	tgatgagccg	catcaccatg	gtcaccagca	ccatgaaggc	60
ataggtgatg	atgaggacat	ggaatgggcc	cccaaggatg	gtctgtccaa	agaagcgagt	120
gacccccatt	ctgaagatgt	ctggaacctc	taccagcagg	atgatgatag	ccccaatgac	180
agtcaccagc	tccccgacca	gccggatata	gtccttaggg	gtcatgtagg	cttccctgaag	240
tagcttctgc	tgtaagaggg	tggtgtcccg	ggggctcggt	cggttattgg	tcctgggctt	300
gagggggcgg	tagatgcagc	acatggtgaa	gcagatgatg	t		341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca	agactcttac	gccccacact	gcaatttggg	cttgttgccg	tatccattta	60
tgtgggcctt	tctcgagttt	ctgattataa	acaccactgg	agcgatgtgt	tgactggact	120
cattcaggga	gctctggttg	caatattagt	t			151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagt	gatacctaag	aaatacctga	aacatatatt	ggcatttata	aatggctcaa	60
atcttcattt	atctctggcc	ttaaccctgg	ctcctgaggg	tgccggccagc	agatcccagg	120
ccagggtct	gttcttgcca	cacctgcttg	a			151

<210> 318
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 318
 actggtggga ggcgctgttt agttggctgt ttccagaggg gtctttcgga gggacctcct 60
 gctgcaggct ggagtgcttt tttcctggc gggagaccgc acattccact gctgaggctg 120
 tgggggcggt ttatcaggca gtgataaaca t 151

<210> 319
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 319
 aactagtggga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta 60
 catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg 120
 taagattggg tttatgtgat tttagtgggt a 151

<210> 320
 <211> 150
 <212> DNA
 <213> Homo sapien

<400> 320
 aactagtggga tccactagtc cagtgtgggt gaattccatt gtgttggggt tctagatcgc 60
 gagcggtgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120
 gagtgttcta cagcttacag taaataccat 150

<210> 321
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 321
 agcaactttg ttttcatcc aggttatattt aggcttagga tttcctctca cactgcagtt 60
 taggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120
 tgctctgag aatcaaagt cttcatacac t 151

<210> 322
 <211> 151
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(151)
 <223> n = A,T,C or G

<400> 322
 atccagcatc ttctcctgtt tcttgcttcc cttttcttcc ttcttasatt ctgcttgagg 60
 tttgggcttg gtcagtttgc cacagggtt ggagatgggt acagtcttct ggcattcggc 120
 attgtgcagg gctcgttca nacttccagt t 151

<210> 323
 <211> 151
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

tgaggacttg	tktttctttt	ctttatttt	aatcctctta	ckttgtaa	atattgccta	60
nagactcant	tactaccag	tttgtgggtt	twtgaggaga	atgtaactgg	acagttagct	120
gttcaatyaa	aaagacactt	ancccatgtg	g			151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

acctgtgtgg	aatttcagct	ttctcatgc	aaaaggattt	tgtatccccg	gcctacttga	60
agaagtggtc	agctaaagga	atccagggtg	ttggttgac	tgtaataacc	tttgatgaaa	120
agagttacta	cgaatcccat	cttggttcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacgggtg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatatcaaaa	taccctttgt	gctaccaggg	ccctggggaa	tcaggtgact	300
cacacaaatg	caatagttgg	tactgcatt	tttacctgaa	ccaaagctaa	acccggtgtt	360
gccaccatgc	accatggcat	gccagagtgc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgccct	agctgangca	c		461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

acactgtttc	catgttatgt	ttctacacat	tgctacctca	gtgctcctgg	aaacttagct	60
tttgatgtct	ccaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgcca	120
agtaagagtg	gtggcctatt	tcagctgctt	tgacaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaaagtc	ccatggtggc	ggcgaagaag	agaaagatgt	240
gttttgtttt	ggactctctg	tggtcccttc	caatgctgtg	ggtttccaac	caggggaagg	300
gtcccttttg	cattgccaag	tgccataacc	atgagcacta	cgctaccatg	gttctgcctc	360
ctggccaagc	aggctgggtt	gcaagaatga	aatgaatgat			400

<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc	agcccgact	cgagccctg	gcaggcgga	ctggtcatgg	aaaacgaatt	60
gttctgctcg	ggcgctcctg	tgcatccgca	gtgggtgctg	tcagccgcac	actgtttcca	120
gaactcctac	accatcgggc	tgggcctgca	cagcttgag	gccgaccaag	agccagggag	180
ccagatggtg	gaggccagcc	tctccgtacg	gcaccagag	tacaacagac	ccttgctcgc	240
taacgacctc	atgctcatca	agttggacga	atccgtgtcc	gagctcgaca	ccatccggag	300
catcagcatt	gcttcgcagt	gccctaccgc	ggggaactct	tgctcgtttt	ctggctgggg	360
tctgctggcg	aacggcagaa	tgctaccgt	gctgcagtgc	gtgaacgtgt	cggtggtgtc	420
tgaggaggtc	tgacgtaagc	tctatgacct	gctgtaccac	cccagcatgt	tctgcgccgg	480
cggagggcaa	gaccagaagg	actcctgcaa	cggtgactct	ggggggcccc	tgatctgcaa	540
cggttacttg	cagggccttg	tgtctttcgg	aaaagccccg	tgtggccaag	ttggcgtgcc	600
aggtgtctac	accaacctct	gcaaattcac	tgagtggata	gagaaaaccg	tccaggccag	660
ttaactctgg	ggactgggaa	cccatgaaat	tgacccccaa	atacatcctg	cggaaggaaat	720
tcaggaatat	ctgttcccag	cccctcctcc	ctcaggccca	ggagtccagg	ccccagccc	780
ctcctccctc	aaaccaaggg	tacagatccc	cagccctccc	tccctcagac	ccaggagtcc	840

97

```

agacccccca gcccctcctc cctcagaccc aggagtccag cccctcctcc ctcagaccca      900
ggagtccaga cccccagcc cctcctccct cagaccaggg ggtccaggcc cccaaccct      960
cctcctcag actcagaggt ccaagccccc aaccctcct tccccagacc cagaggtcca      1020
ggtcccagcc cctcctccct cagaccagc ggtccaatgc cacctagact ctccctgtac      1080
acagtcccc cttgtggcac gttgacccaa ccttaccagt tggtttttca tttttgtcc      1140
ctttccccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaaa aaaaaaaaaa      1200
aaaaaaaaaa aaaaaa                                     1215

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<210> 327
 <211> 220
 <212> PRT
 <213> Homo sapien

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<400> 327
Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1          5          10          15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
 20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
 35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
 50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
 65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
 85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
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Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
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Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165          170          175
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Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
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 <212> DNA
 <213> Homo sapien

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 <212> PRT
 <213> Homo sapien

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<400> 329
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 <212> DNA
 <213> Homo sapien

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 <213> Homo sapien

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<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

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<211> 2417

<212> DNA

<213> Homo sapien

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<211> 2984

101

<212> DNA

<213> Homo sapien

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<210> 336

<211> 147

<212> PRT

<213> Homo sapien

<400> 336

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102

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      130          135          140
Ala Phe Trp
145

```

```

<210> 337
<211> 9
<212> PRT
<213> Homo sapien

```

```

      <400> 337
Ala Leu Thr Gly Phe Thr Phe Ser Ala
      1           5

```

```

<210> 338
<211> 9
<212> PRT
<213> Homo sapien

```

```

      <400> 338
Leu Leu Ala Asn Asp Leu Met Leu Ile
      1           5

```

```

<210> 339
<211> 318
<212> PRT
<213> Homo sapien

```

```

      <400> 339
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
      1           5           10           15
Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
      20           25           30
Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
      35           40           45
Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
      50           55           60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
      65           70           75           80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
      85           90           95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
      100          105          110
Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
      115          120          125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met

```

130	135	140
His Ile Gly Val Asn His	Leu Gly His Phe Leu Leu Thr His Leu Leu	
145	150	155
Leu Glu Lys Leu Lys Glu	Ser Ala Pro Ser Arg Ile Val Asn Val Ser	160
	165	170
Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly		175
	180	185
Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala		190
	195	200
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly		205
	210	215
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val		220
225	230	235
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe		240
	245	250
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu		255
	260	265
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His		270
	275	280
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg		285
	290	295
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp		300
305	310	315

<210> 340
 <211> 483
 <212> DNA
 <213> Homo sapien

<400> 340
 gccgaggtct gccttcacac ggaggacacg agactgcttc ctcaagggct cctgcctgcc 60
 tggacactgg tgggaggcgc tggttagttg gctgttttca gagggggtctt tcggaggggac 120
 ctctgctgctc aggtctggagt gtctttattc ctggcggggag accgcacatt ccaactgctga 180
 ggttggtgggg gcggtttatc aggcagtgat aaacataaga tgctatttcc ttgactccgg 240
 ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgacccct 300
 gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttgggtcacg 360
 tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt 420
 tttctgggc ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480
 ctg 483

<210> 341
 <211> 344
 <212> DNA
 <213> Homo sapien

<400> 341
 ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc 60
 tatttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct 120
 gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca 180
 attaatttaa taatttctga tgatggtttt atctgcagta atatgtatat catctattag 240
 aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300
 ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342
 <211> 592
 <212> DNA
 <213> Homo sapien

<400> 342
 acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac 60
 caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca 120
 cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg 180

104

```

accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact 240
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat ttttaattggc 300
aagtgccact gtggaaagag ttctgtgtg tgctgaagtt ctgaagggca gtcaaattca 360
tcagcatggg ctgtttgggtg caaatgcaaa agcacaggtc tttttagcat gctgggtctct 420
cccggtgcct tatgcaaata atcgtcttct tctaaatttc tcctaggctt cattttccaa 480
agttcttctt ggtttggat gtcttttctg ctttccatta attctataaa atagtatggc 540
ttcagccacc cactcttcgc cttagcttga ccgtgagtct cggctgccgc tg 592

```

<210> 343

<211> 382

<212> DNA

<213> Homo sapien

<400> 343

```

ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt 60
cttaatgttt gtggctttct ctccagcctc tcttaggagg ggtaatgggt gagttggcat 120
cttgtaactc tcctttctcc tttcttcccc tttctctgcc cgcctttccc atcctgctgt 180
agactttctg attgtcagtc tgtgtcacat ccagtgattg ttttggttcc tgttcccttt 240
ctgactgccc aaggggctca gaaccccagc aatcccttcc tttcactacc ttcttttttg 300
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaagagg 360
aaaccaccaa gctgaaaaaa aa 382

```

<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

```

ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga 60
caataggcca cataaacttg gctggatgga acctcacaat aagggtgtca cctcttgttt 120
gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca 180
agcttttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc 240
caccttcatg tgctgaatg gttgccaggt cagaaaaatc cacccttac gagtgcggt 300
tcgacctat atcccccgcc cgcgtccctt tctccataaa attcttctta gtagctatta 360
cttcttatt attgatcta gaaattgcc tcttttacc cctaccatga gccctacaaa 420
caactaacct gccactaata gttatgtcat ccctcttatt aatcatcatc ctagccctaa 480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa 536

```

<210> 345

<211> 251

<212> DNA

<213> Homo sapien

<400> 345

```

accttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg 60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg 120
gcgtggggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga 180
aaataacata tcgattttgg agagacactg ccaactggct ggagattaat ccggacactg 240
gtgccatttc c 251

```

<210> 346

<211> 282

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(282)

<223> n = A,T,C or G

<400> 346

```

cgcgctctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60

```

```

ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga 120
agggagacta tacctggctc ttgccctaag tgagaggctt tccctcccgc accaaaaaat 180
agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg 240
ggtctcattt cccaagggtc cttcaatgct catnaaaacc aa 282

```

```

<210> 347
<211> 201
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

```

```

<400> 347
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
taaataaac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tctgagactg actggacca cccagacca gggcaaagat acatgttacc atatcatctt 180
tataaagaat tttttttgt c 201

```

```

<210> 348
<211> 251
<212> DNA
<213> Homo sapien

```

```

<400> 348
ctgttaatca caacatttgt gcatacttg tgccaagtga gaaaatgttc taaaatcaca 60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
aggagacact cccagcatgg aggagggtt atcttttcat cctaggtcag gtctacaatg 180
ggggaagggt ttattataga actccaaca gcccacctca ctctgtccac ccacccgatg 240
gccctgcctc c 251

```

```

<210> 349
<211> 251
<212> DNA
<213> Homo sapien

```

```

<400> 349
taaaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac 60
aaccctgag gatgccagag ctatgggtcc agaacatggt gtggtattat caacagagtt 120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca 240
actcctggtt t 251

```

```

<210> 350
<211> 908
<212> DNA
<213> Homo sapien

```

```

<400> 350
ctggacactt tgcgagggtt tttgctggct gctgctgctg cccgtcatgc tactcatcgt 60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac 120
cggctggaat tgctctggtt atgatgacag agaaaatgat ctcttcctct gtgacaccaa 180
cactgtaaa tttgatggg aatgtttaag aattggagac actgtgactt gcgtctgtca 240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa 300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tgggtgcaga 360
aggatcatgt gccacagtcc atgaaggctc tggagaaact agtcaaaagg agacatccac 420
ctgtgatatt tgccagtttg gtgcagaatg tgacgaagat gccgaggatg tctggtgtgt 480
gtgtaatatt gactgttctc aaaccaactt caatcccctc tgcgcttctg atgggaaatc 540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aaattgaagt 600
catgtctttg ggtcgatgct aagataaac aactacaact actaagtctg aagatgggca 660

```

ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagt	ccagagaaca	720
ccacatacct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgacagtg	tgatgctgg	tatactggac	aacactgtga	840
aaaaaggac	tacagtgttc	tatacgttgt	tcccggctct	gtacgatttc	agtatgtctt	900
aatcgacg						908

<210> 351
 <211> 472
 <212> DNA
 <213> Homo sapien

<400> 351						
ccagttat	gcaagtgg	agagcctat	taccataaat	aataactaaga	accaaactcaa	60
gtcaaacc	aatgccatt	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaact	attttaaa	cagwtttgyg	agtcatttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccatt	tattcctgtt	tttctaataa	gtcctaattt	ctaacactgt	240
atatatcctt	cgacatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgcttc	tcaccatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttagggaag	atgttgcttt	gccacacac	gaagcaaagt	aa	472

<210> 352
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 352						
ctcaaagcta	atctctcggg	aatcaaacca	gaaaagggca	aggatcttag	gcatgggtgga	60
tgtggataag	gccaggtcaa	tggtgcaag	catgcagaga	aagaggtaca	tcggagcgtg	120
caggctgcgt	tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaacca	gaaatgggct	ttctctaate	ctgggatacc	240
aataagcaca	a					251

<210> 353
 <211> 436
 <212> DNA
 <213> Homo sapien

<400> 353						
ttttttttt	ttttttttt	ttttttacaa	caatgcagtc	atttatttat	tgagtatgtg	60
cacattatgg	tattattact	atactgatta	tatttatcat	gtgacttcta	attaraaaat	120
gtatccaaaa	gcaaaacagc	agatatataa	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacatt	gacaatccaa	atccaataca	tttaaacatt	tgaggaaatga	240
gggggacaaa	tggaagccar	atcaaatttg	tgtaaaacta	ttcagtatgt	ttcccttgct	300
tcatgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
ttaacagaat	actagattca	cactggaacg	ggggtaaaga	agaaattatt	ttctataaaa	420
gggctcctaa	tgtagt					436

<210> 354
 <211> 854
 <212> DNA
 <213> Homo sapien

<400> 354						
ccttttctag	ttcaccagtt	ttctgcaagg	atgctgggta	gggagtgtct	gcaggaggag	60
caagtctgaa	accaaatcta	ggaaaacatag	gaaacgagcc	aggcacagg	ctgggtgggc	120
atcagggacc	accctttggg	ttgatatttt	gcttaatctg	catcttttga	gtaagatcat	180
ctggcagtag	aagctgttct	ccaggtacat	ttctctagct	catgtacaaa	aacatcctga	240
aggactttgt	caggtgcctt	gctaaaagcc	agatgcgttc	ggcacttcct	tggtctgagg	300
ttaattgcac	acctacaggc	actgggctca	tgctttcaag	tattttgtcc	tcacttttagg	360
gtgagtga	gatccccatt	ataggagcac	ttgggagaga	tcataataaa	gctgactctt	420
gagtacatgc	agtaatgggg	tagatgtgtg	tggtgtgtct	tcattcctgc	aagggtgctt	480

```

gtagggagt gtttccagga ggaacaagtc tgaaccaaat catgaaataa atggtagggtg 540
tgaactggaa aactaattca aaagagagat cgtgatatca gtgtgggtga tacaccttgg 600
caatatggaa ggctctaatt tgcccatatt tgaataataa attcagcttt ttgtaataca 660
aaataacaaa ggattgagaa tcatgggtgc taatgtataa aagaccagc aacataaat 720
atatcaactg cataaatgta aaatgcatgt gacccaagaa ggcacaaaag tggcagacaa 780
cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc 840
acacgggatg tcag 854

```

<210> 355
 <211> 676
 <212> DNA
 <213> Homo sapien

```

<400> 355
gaaattaagt atgagctaaa ttccctgtta aaacctctag gggtgacaga tctcttcaac 60
caggtcaaag ctgatctttc tggaatgtca ccaaccaagg gcctatattt atcaaaagcc 120
atccacaagt catacctgga tgcagcgaa gagggcacgg aggcagcagc agccactggg 180
gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccaccttctc 240
ctgttcttta taaggcacac tcataccaac acgatcctat tctgtggcaa gcttgccctc 300
ccctaatacag atgggggtga gtaaggctca gagttgcaga tgaggtgcag agacaatcct 360
gtgactttcc cacggccaaa aagctgttca cacctcacgc acctctgtgc ctgagtttgc 420
tcactcgcaa aataggtcta ggattcttc caaccatttc atgagttgtg aagctaaggc 480
ttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt 540
ggtgtctcat ttgagtgtcg tccagtgtga tgatcaagtc aatgagtaaa attttaaggg 600
attagatttt cttgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct 660
gcttaaagaa aaccag 676

```

<210> 356
 <211> 574
 <212> DNA
 <213> Homo sapien

```

<400> 356
ttttttttt ttttccagga aaacattctc ttactttatt tgcattctcag caaaggttct 60
catgtggcac ctgactggca tcaaaccaaa gttcgtaggc caacaaagat gggccactca 120
caagcttccc attttagat ctgagtcct atgagtatct gacacctgtt cctctcttca 180
gtctcttagg gaggtttaa tctgtctcag gtgtgctaag agtgccagcc caaggkgtc 240
aaaagtccac aaaactgcag tctttgctgg gatagtaagc caagcagtgc ctggacagca 300
gagttctttt cttgggcaac agataaccag acaggactct aatcgtgctc ttattcaaca 360
ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acagggaagg 420
agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctgtctg 480
gatagacggc acaggagct cttagggtcag cgctgctggg tggaggacat tctgagtc 540
agctttgcag cctttgtgca acagtacttt ccca 574

```

<210> 357
 <211> 393
 <212> DNA
 <213> Homo sapien

```

<400> 357
ttttttttt ttttttttt ttttttttt tacagaatat aratgcttta tcaactgkact 60
taatatggkg kcttggtcac tatacttaaa aatgcaccac tcataaatat ttaattcagc 120
aagccacaac caaracttga ttttatcaac aaaaaccctt aaatataaac ggsaaaaaag 180
atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara 240
araarataag tggttatagg aaagaagggc attcaagcac actaaaraaa cctgaggkaa 300
gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct 360
ttttttctt tttctgtttt ttttttttt tac 393

```

<210> 358
 <211> 630
 <212> DNA
 <213> Homo sapien

<400> 358
 acagggtaaa caggaggatc cttgctctca cggagcttac attctagcag gaggacaata 60
 ttaatgttta taggaaaatg atgagtttat gacaaaggaa gtagatagtg ttttacaaga 120
 gcatagagta ggaagctaa tccagcacag ggaggtcaca gagacatccc taaggaagtg 180
 gagtttaaac tgagagaagc aagtgcctaa actgaaggat gtgttgaaaga agaagggaga 240
 gtagaacaat ttgggcagag ggaaccttat agaccctaag gtgggaaggt tcaagaact 300
 gaaagagagc tagaacagct ggagccgttc tccggtgtaa agaggagtca aagagataag 360
 attaaagatg tgaagattaa gatcttggtg gcattcaggg attggcactt ctacaagaaa 420
 tctactgaag gagtaatgtg acattacttt tcaattcagg atggccattc taactccagg 480
 gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcgatagt 540
 gaaagacaaa aataagtggg gaaattcagg ggatagtga aatcagtagg acttaatgag 600
 caagccagag gttcctccac aacaaccagt 630

<210> 359
 <211> 620
 <212> DNA
 <213> Homo sapien

<400> 359
 acagcattcc aaaaatataca tctagagact aarrgtaaat gctctatagt gaagaagtaa 60
 taattaaaaa atgctactaa tatagaaaat ttataatcag aaaaataaat attcagggag 120
 ctcaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat 180
 atggcattcc ccaagggaaa tagagagatt cttctggatt atgttcaata tttatttcac 240
 aggattaact gttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac 300
 aaagacaaca tgatacctta ggaagcaaca ctaccctttc aggcataaaa tttggagaaa 360
 tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt 420
 aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca 480
 aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca 540
 aacaaaaagc tcacaccaaa caaaaccatc aacttatitt gtattctata acatacgaga 600
 ctgtaaagat gtgacagtgt 620

<210> 360
 <211> 431
 <212> DNA
 <213> Homo sapien

<400> 360
 aaaaaaaaaa agccagaaca acatgtgata gataatatga ttggctgcac acttccagac 60
 tgatgaatga tgaacgtgat ggactattgt atggagcaca tcttcagcaa gagggggaaa 120
 tactcatcat ttttgccag cagttgtttg atcaccaaac atcatgccag aatactcagc 180
 aaaccttctt agctcttgag aagtcaaagt ccgggggaat ttattcctgg caattttaat 240
 tggactcctt atgtgagagc agcggctacc cagctggggt ggtggagcga acccgctact 300
 agtggacatg cagtggcaga gctcctggtg accacctaga ggaatacaca ggcacatgtg 360
 tgatgccaag cgtgacacct gtagcactca aatttgtctt gtttttgtct ttcggtgtgt 420
 agattcttag t 431

<210> 361
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 361
 aacttgattt ccgatcaaaa gaatcatcat ctttaccttg acttttcagg gaattactga 60
 actttcttct cagaagatag ggcacagcca ttgccttggc ctcacttgaa gggctctgcat 120
 ttgggtcctc tggctctctt ccaagtttcc cagccactcg agggagaaat atcgggaggt 180
 ttgacttccct ccggggcttt cccgagggtt tcaccgtgag ccctgcggcc ctacgggctg 240
 caatcctgga ttcaatgtct gaaacctcgc tctctgctcg ctggacttct gaggccgtca 300
 ctgccactct gtcctccagc tctgacagct cctcatctgt ggtcctgttg t 351

<210> 362
 <211> 463

109

<212> DNA

<213> Homo sapien

<400> 362

acttcatcag gccataatgg gtgcctcccg tgagaatcca agcacctttg gactgcgcga	60
tgtagatgag ccggctgaag atcttgcgca tgcgcggctt cagggcggaag ttcttggcgc	120
ccccggtcac agaaatgacc aggttgggtg ttttcagggtg ccagtgcgtg gtcagcagct	180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttcctt ttcttcccca	240
gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttcttgggtg tgtttcttgt	300
agttccattt ctacttttgg ttgatctggg tgccttccat gtgctggctc tgggcatagc	360
cacacttgca cacattctcc ctgataagca cgatggtgtg gacaggaagg aaggatttca	420
ttgagcctgc ttatggaaac tggattgtt agcttaaata gac	463

<210> 363

<211> 653

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 363

acccccgagt nctgntctgg catactgnga acgaccaacg acacacccaa gctcggcctc	60
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tgggaggcac tacgcaagat gggactgcgt cctgggggtga gacatcctct ccttgagat	180
ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc	240
ccaacagcaa cccccggaa gtatgagttc ctctrgggcc tccgttcta ccatgagasc	300
tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact	360
ggtctgcaca gttcatggag gctgcagatg aggccttggg tgctctggat gctgctgcag	420
ctgaggccga agcccgggct gaagcaagaa cccgcatggg aattggagat gaggctgtgt	480
ntgggccctg gagctgggat gacattgagt ttgagctgct gacctgggat gagggaaggag	540
attttgagga tccntgggtc agaattccat ttaccttctg gccagatac caccagaatg	600
cccgtccag attccctcag acctttgccg gtcccattat tggtcstggt ggt	653

<210> 364

<211> 401

<212> DNA

<213> Homo sapien

<400> 364

actagaggaa agacgttaaa ccactctact accacttgtg gaactctcaa agggtaaattg	60
acaaagccaa tgaatgactc taaaaacaat atttacattt aatggtttgt agacaataaa	120
aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga	180
tgagaaaagct caattataga tgcaaaagta taactaaact actatagtag taaagaaata	240
catttcacac cttcatata aattcactat cttggcttga ggcactccat aaaatgtatc	300
acgtgcatag taaatcttta tatttgctat ggcgttgcac tagaggactt ggactgcaac	360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g	401

<210> 365

<211> 356

<212> DNA

<213> Homo sapien

<400> 365

ccagtgtcat atttgggctt aaaatttcaa gaagggcact tcaaattggct ttgcatttgc	60
atgtttcagt gctagagcgt aggaatagac cctggcgctc actgtgagat gttcttcagc	120
taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa	180
ctctccatcc cctggctttg gcttcggcct tgcgttttgc gcatcatctc cgtaaatggt	240
gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga	300
acattcggca atgtcccctt ttagccagat ttcttcttcg agctcccga gagcag	356

110

<210> 366
 <211> 1851
 <212> DNA
 <213> Homo sapien

<400> 366

tcataccat	tgccagcagc	ggcaccgtta	gtcagggtttt	ctgggaatcc	cacatgagta	60
cttcctgtt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tcaacttctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
ttgctgtttt	cagaagagat	ttttaacatc	tgtttttctt	tgtagtcaga	aagtaactgg	240
caaattacat	gatgatgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacattttgc	tcaagtagag	ggctgactat	acttgctgat	ccacaacata	360
cagcaagtat	gagagcagtt	cttccatata	tatccagcgc	atttaaattc	gcttttttct	420
tgattaaaaa	tttcaccact	tgctgttttt	gctcatgtat	accaagtagc	agtggtgtga	480
ggccatgctt	gttttttgat	tcgatatcag	caccgtataa	gagcagtgtc	ttggccatta	540
atttatcttc	attgtagaca	gcatagtgta	gagtggtatt	tccatactca	tctggaatat	600
ttggatcagt	gccatgttcc	agcaacatta	acgcacattc	atcttcctgg	cattgtacgg	660
cctttgtcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	cgtctgtcca	720
gcacgagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	gcagtccctc	780
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acagaggatg	agatccagaa	accacaatat	ccattcacaa	acaaacactt	ttcagccaga	1260
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ccagtcgcag	agaagccaca	ctgaagctct	gtcctcagcc	atcagcgcca	cggacaggag	1500
tgtgtttctt	ccccagtgat	gcagcctcaa	gttatcccga	agctgccgca	gcacacggtg	1560
gctcctgaga	aacaccccag	ctcttcgggt	ctaacacagg	caagtcaata	aatgtgataa	1620
tcacataaac	agaattaaaa	gcaaagtcac	ataagcatct	caacagacac	agaaaaggca	1680
tttgacaaaa	tcagcatccc	ttgtatttat	tggtgcagtt	ctcagaggaa	atgcttctaa	1740
cttttcccca	tttagtatta	tggtggctgt	gggcttgtca	taggtgggtt	ttattacttt	1800
aaggtatgtc	ccttctatgc	ctgttttgct	gagggtttta	attctcgtgc	c	1851

<210> 367
 <211> 668
 <212> DNA
 <213> Homo sapien

<400> 367

cttgagcttc	caaataygga	agactggccc	ttacacasgt	caatgttaaa	atgaatgcat	60
ttcagtatct	tgaagataaa	atttgtatag	ctataccttg	ttttttgatt	cgatatcagc	120
accrtataag	agcagtgtct	tgccatttaa	tttatctttc	attttagaca	gcrtagtgya	180
gagtggtatt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttcctgg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccac	cctcatgctg	atatagtgg	420
ctactgcata	cctttatcag	agctgtcctc	tttttggtgt	caaggacatt	aagttgacat	480
cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
gcaatgatcc	atgtaactgc	aaacactgaa	tagcctgtca	ttactctgcc	ttcaaaaaaa	660
aaaaaaa						668

<210> 368
 <211> 1512
 <212> DNA
 <213> Homo sapien

<400> 368

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tgggctgggc	trgaatcccc	tgctgggggtt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagttggt	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgtaaaaagc	agatgggtgt	tgaggttgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
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ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagt	600
gccttcctgg	agcccaggta	ccacgtccgt	ggagaagatc	tggacaagct	ccacagagct	660
gcctggtggg	gtaaagtccc	cagaaaggat	ctcatcgta	tgctcaggga	cactgacgtg	720
aacaagaagg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgcca	tgggaattca	780
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gaacatggca	ctgatccaaa	tattccagat	gagtaggaa	ataccactct	rcactaygct	960
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gaaaacactg	aatttgtaaa	aggtaatact	tactattttt	caatttttcc	ctcctaggat	1320
ttttttcccc	taatgaatgt	aagatggcaa	aatttgcctt	gaaataggtt	ttacatgaaa	1380
actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
taaaaaacag	taatagatac	gaggtgatgc	gcctgtcagt	ggcaaggttt	aagatatttc	1500
tgatctcgtg	cc					1512

<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

gggtcgccca	ggggsgcgt	gggctttcct	cggttgggtg	tgggttttcc	ctgggtgggg	60
tgggctgggc	trgaatcccc	tgctgggggtt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagttggt	gaaactgggt	ggtagacgcg	180
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tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
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gccttcctgg	akcccaggta	ccacgtccrt	ggagaagatc	tggacaagct	ccacagagct	660
gcctggtggg	gtaaagtccc	cagaaaggat	ctcatcgta	tgctcaggga	cackgaygtg	720
aacaagargg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgcca	tgggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
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gaacatggca	ctgatccaaa	tattccagat	gagtaggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tatayggtgc	tgatatcgaa	1020
tcaaaaaaca	agcatggcct	cacaccactg	ytacttggtt	tacatgagca	aaaacagcaa	1080
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gcaaaatr	gatgtatctt	ctcaagatct	ggaaagacgg	ccagagagta	tgctgtttct	1260
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ttttggttta	atgttttttt	tttttgcctt	aataatatta	gatagtcca	aatgaaatwa	1500
cctatgagac	taggctttga	gaatcaatag	attctttttt	taagaatctt	ttggctagga	1560
gcggtgtctc	acgcctgtaa	ttccagcacc	ttgagaggct	gaggtgggca	gatcacgaga	1620

112

tcaggagatc	gagaccatcc	tggctaacac	ggtgaaaccc	catctctact	aaaaatacaa	1680
aaacttagct	gggtgtggtg	gcgggtgcct	gtagtcacag	ctactcagga	rgctgaggca	1740
ggagaatggc	atgaacccgg	gaggtggagg	ttgcagttag	ccgagatccg	ccactacact	1800
ccagcctggg	tgacagagca	agactctgtc	tcaaaaaaaaa	aaaaaaaaaaa	aaa	1853

<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

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tttctcttga	gaactgcaac	aataaataca	aggatgctgg	attttgtcaa	atgccttttc	180
tgtgtctgtt	gagatgctta	tgtgactttg	cttttaattc	tgtttatgtg	attatcacat	240
ttattgactt	gcctgtgtta	gaccggaaga	gctgggggtg	ttctcaggag	ccaccgtgtg	300
ctgcggcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytctgtcc	360
gtggcgctga	tggctgagga	cagagcttca	gtgtggcttc	tctgcgactg	gcttcttcgg	420
ggagttcttc	cttcatagtt	catccatatg	gctccagagg	aaaattatat	tattttgtta	480
tggatgaaga	gtattacgtt	gtgcagatat	actgcagtgt	cttcactctt	tgatgtgtga	540
ttgggtaggt	tccaccatgt	tgccgcagat	gacatgattt	cagtacctgt	gtctggctga	600
aaagtgtttg	tttgtgaatg	gatattgtgg	tttctggatc	tcactctctg	tggggtggaca	660
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ccatcgtgca	tgcatctttc	atttcctgca	tttcttcttc	cctggatgga	cagggggagc	780
ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	gacgcttggg	840
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acgtggtcgc	ttggggagac	tacgatgaca	gcgccttcat	ggatcccagg	taccacgtcc	960
atggagaaga	tctggacaag	ctccacagag	ctgcctgggtg	gggtaaagtc	cccagaaagg	1020
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ctctacatct	ggcctctgcc	aatgggaatt	cagaagtagt	aaaactcgtg	ctggacagac	1140
gatgtcaact	taatgtcctt	gacaacaaaa	agaggacagc	tctgacaaag	gccgtacaat	1200
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<210> 371

<211> 1855

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(1855)

<223> n = A,T,C or G

<400> 371

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cacgcgcacg	ttgcacgcgc	ggcagcggct	tggtgtgctt	gtaacggctt	gcacgcgcac	120

113

gccgcccccg	cataaccgct	agactggcct	gtaacggctt	gcaggcgcac	gccgcacgcg	180
cgtaacggct	tggctgccct	gtaacggctt	gcacgtgcat	gctgcacgcg	cgttaacggc	240
ttggctggca	tgtagccgct	tggcttggct	ttgcattytt	tgctkggctk	ggcgttgkty	300
tcttgattg	acgcttcctc	cttgatkgga	cgtttcctcc	ttgatkgac	gtttcytyty	360
tcgcgttcct	ttgctggact	tgacctttty	tctgctgggt	ttggcattcc	tttgggggtg	420
gctgggtggt	ttctccgggg	gggkktgccc	ttcctggggg	gggcgtgggk	cgccccagg	480
gggcgtgggc	tttccccggg	tgggtgtggg	ttttcctggg	gtgggggtgg	ctgtgctggg	540
atccccctgc	tggggttggc	agggattgac	ttttttcttc	aaacagattg	gaaacccgga	600
gtaacntgct	agtgggtgaa	actggttggt	agacgcgac	tgctgttact	actgtttctc	660
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agaagccatt	tggctcagc	agcaagatgg	gcaagtgggt	cgccactgct	tcccctgctg	780
caggggggagc	ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	840
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cggaagagc	aacgtggkcg	cttggggaga	ctacgatgac	agcgcttca	tggakcccag	960
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agggccagtc	ttccgtatct	ggaagctcaa	gcataacttg	aatgaaaata	ttttgaaatg	1500
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cagttttttt	tttttaaatg	cacttctggt	aaatactttt	gttgaaaaca	ctgaatttgt	1620
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tgtaagatgg	caaaatttgc	cctgaaatag	gttttacatg	aaaactccaa	gaaaagttaa	1740
acatgtttca	gtgaatagag	atcctggtcc	tttggaaggt	tcctaaaaaa	cagtaataga	1800
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<210> 372

<211> 1059

<212> DNA

<213> Homo sapien

<400> 372

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gcgcttgrg	agactmcgat	gacagygcct	tcatggagcc	caggtaccac	gtccgtggag	180
aaagatctgga	caagctccac	agagctgccc	tggtggggta	aagtccccag	aaaggatctc	240
atcgctcatg	tcagggacac	tgaygtgaac	aagarggaca	agcaaaaagag	gactgctcta	300
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caacttaatg	tccttgacaa	caaaaagagg	acagctctga	yaaaggccgt	acaatgccag	420
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<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

<400> 373

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<210> 374

<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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<210> 375

115

<211> 2040

<212> DNA

<213> Homo sapien

<400> 375

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<210> 376

<211> 329

<212> PRT

<213> Homo sapien

<400> 376

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			20					25					30		
Glu	Tyr	Thr	Ile	Val	His	Ala	Ser	Phe	Ile	Ser	Cys	Ile	Ser	Ser	Ser
		35					40					45			
Leu	Asp	Gly	Gln	Gly	Glu	Arg	Gln	Glu	Gln	Arg	Gly	His	Phe	Trp	Arg
	50					55				60					
Pro	Gln	Arg	Leu	Leu	Cys	Glu	Asp	Ala	Trp	Glu	Gln	Glu	Val	Gln	Val
65					70				75					80	
Val	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Gln	Gly	Ser	Gly	Lys	Ser	Asn	Val
			85					90						95	
Val	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	Met	Asp	Pro	Arg	Tyr
			100					105					110		
His	Val	His	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp
			115					120						125	

116

Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
 130 135 140
 Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
 145 150 155 160
 Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
 165 170 175
 Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
 180 185 190
 Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
 195 200 205
 Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
 210 215 220
 Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
 225 230 235 240
 Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
 245 250 255
 Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
 260 265 270
 Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
 275 280 285
 Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
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 305 310 315 320
 Ser Met Leu Phe Leu Val Ile Ile Met
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<210> 377
 <211> 148
 <212> PRT
 <213> Homo sapien

<220>
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 <223> Xaa = Any Amino Acid

<400> 377
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 20 25 30
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
 35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT

<213> Homo sapien

<400> 378

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Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35          40          45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50          55          60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65          70          75          80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85          90          95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100          105          110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115          120          125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130          135          140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145          150          155          160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165          170          175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180          185          190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195          200          205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210          215          220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225          230          235          240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245          250          255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260          265          270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275          280          285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290          295          300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305          310          315          320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325          330          335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val
 340          345          350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355          360          365
Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
 370          375          380
Pro Arg Thr His Met Val Glu Val Asp Ser Met Pro Ala Ala Ser
 385          390          395          400
Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
 405          410          415
Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
 420          425          430
Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
 435          440          445
Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
 450          455          460
Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys

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465					470					475					480
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Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp
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Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu
		515					520					525			
Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp
	530				535						540				
Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln
545					550					555					560
Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val
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Val	Lys	Leu	Leu	Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn
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Lys	Lys	Arg	Thr	Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu
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	610					615					620				
Glu	Tyr	Gly	Asn	Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys
625					630					635					640
Leu	Met	Ala	Lys	Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys
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Asn	Lys	His	Gly	Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys
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Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala
		675					680					685			
Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly
	690					695					700				
Ser	Ala	Ser	Ile	Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser
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Ser	Gln	Asp	Leu	Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser
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His	His	His	Val	Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln
			740					745					750		
Met	Leu	Lys	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys
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Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser
	770					775					780				
Gln	Pro	Glu	Lys	Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp
785					790					795					800
Arg	Glu	Val	Glu	Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly
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 980 985 990
 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
 995 1000 1005
 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
 1010 1015 1020
 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
 1025 1030 1035 104
 Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
 1045 1050 1055
 Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
 1060 1065 1070
 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
 1075 1080 1085
 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
 1090 1095 1100
 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
 1105 1110 1115 112
 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
 1125 1130 1135
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 1170 1175 1180
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 1185 1190 1195 120
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 Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
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 1235 1240 1245
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 1250 1255 1260
 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
 1265 1270 1275 128
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 1285 1290 1295
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
 1300 1305 1310
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
 1315 1320 1325
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
 1330 1335 1340
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
 1345 1350 1355 136
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
 1365 1370 1375
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
 1380 1385 1390
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
 1395 1400 1405
 Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
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 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
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 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
 1445 1450 1455
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser

120

1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 152
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 160
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 168
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
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 Met Lys His Gln Ser Gln Leu
 1715

<210> 379
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 379
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 1 5 10 15
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 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175

Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
 515 520 525
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
 530 535 540
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
 545 550 555 560
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
 565 570 575
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
 580 585 590
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
 595 600 605
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
 610 615 620
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
 625 630 635 640
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 645 650 655

<210> 380

122

<211> 671
 <212> PRT
 <213> Homo sapien

<400> 380

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			20					25					30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp
		35					40					45			
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp
	50					55					60				
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val
65					70				75					80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn
				85					90					95	
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser
			100					105					110		
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe
		115					120					125			
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His
	130					135					140				
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
145					150					155				160	
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala
			165						170					175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu
		180						185					190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
		195					200					205			
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met
	210					215					220				
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn
225					230					235					240
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys
				245					250					255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly
		260						265					270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val
		275					280					285			
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr
	290					295					300				
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
305					310					315					320
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
				325					330					335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
			340					345					350		
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu
	370					375					380				
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys
385					390					395				400	
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu
				405					410					415	
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu	Asn
			420					425					430		
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile	Pro
		435					440					445			
Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	Pro	Asp	Asn	Glu

450		455		460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu				
465		470		480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp				
	485		490	495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu				
	500		505	510
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp				
	515		520	525
Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys				
	530		535	540
His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala				
	545		550	555
Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg				
	565		570	575
Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His				
	580		585	590
Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn				
	595		600	605
Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile				
	610		615	620
Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys				
	625		630	635
Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala				
	645		650	655
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu				
	660		665	670

<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381	
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ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg	120
ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac	180
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caagcagtca g	251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

<400> 382	
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cactggggagg ggacatcctg cagaaggtag gagtgcagaa acacccgctg caggggaggg	180
gagagccctg cggcacctg gggagcagag ggagcagcac ctgcccaggc ctgggaggag	240
ggccttgagg ggcgtgagga ggagcgaggg ggctgcatgg ctggagttag ggatcagggg	300
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aagaaggaca gggcctggct cagggtgtcca gaggctgtcg ctggcttccc tttgggatca	480
gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg	540
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cctcagttct tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact	660
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gcacatctga gatgggtccc gccctcatcc tgctgacctg tctgcaggga ctgtcctcct	840
ggaccttgcc ccttggtgcag gagctggacc ctgaagtccc ctcccatag gccaaagactg	900
gagccttggt ccctctgttg gactccctgc ccatattctt gtgggagtggt gttctggaga	960

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ttacccttag	ggtgattctg	ggggtccact	tgtctgtaat	ggtgtgcttc	aaggtatcac	1140
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taggggggaga	aactgaaagc	tgattaatta	caggaggttt	gttcaggttc	cccaaaccac	1860
cgtcagattt	gatgatttcc	tagcaggact	tacagaaata	aagagctatc	atgctgtggt	1920
ttattattggt	ttgttacact	gataggatata	atactgaaat	cagcaaacaa	aacagatgta	1980
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caaggtatga	tgataatatg	tcaaaagtta	ttccaactga	ggaagctcac	ctgatcctta	2280
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cagatgtaca	aaaacaggga	ttcatcacaa	atcccatctt	tagcatgaag	gggtctggcat	2460
ggcccaaggc	cccaagtata	tcaaggcata	tgggcagaac	atgccaaagg	atcaaattgc	2520
atctcccagg	agttattcaa	gggtgagccc	tttactttgg	atgtacaggc	tttgagcagt	2580
cgaggggctgc	ttagtcaacc	ttttattgta	cagggtatga	gggaaggagg	gaggatgagg	2640
aagccccccct	ggggatttgg	tttgggtctt	tgatcagggt	gtctatgggg	ctatccctac	2700
aaagaagaat	ccagaaatag	gggcacattg	aggaatgata	ctgagcccaa	agagcattca	2760
atcattgttt	tatttgcctt	cttttcacac	cattgggtgag	ggagggatta	ccaccctggg	2820
gttatgaaga	tggttgaaca	ccccacacat	agcaccggag	atatgagatc	aacagtttct	2880
taccatagata	gattcacagc	ccagagcagg	aggacgctgc	acaccatgca	ggatgacatg	2940
ggggatgctc	tccggattgg	tgtgaagaag	caaggactgt	tagaggcagg	ctttatagta	3000
acaagacgggt	ggggcaaact	ctgattttccg	tgggggaatg	tcatggtctt	gctttactaa	3060
gtttttgagac	tggcagggtag	tgaaaactcat	taggctgaga	accttgtgga	atgcagctga	3120
cccagctgat	agaggaagta	gccaggtggg	agcctttccc	agtgggtgtg	ggacatatct	3180
ggcaagatttt	tgtggcactc	ctggtttacg	atactggggc	agcaaataaa	actgaatctt	3240
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<210> 383
<211> 155
<212> PRT
<213> Homo sapiens
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<400> 383
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      5                                10                                15

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
      20                                25                                30

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
      35                                40                                45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
      50                                55                                60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
      65                                70                                75                                80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala

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125

85 90 95

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
100 105 110

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
115 120 125

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
130 135 140

Ala Leu Glu Arg Gly His Leu Val Arg Glu
145 150

<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

<400> 384

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aaagatgtgt ttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cccttttgca ttgccaagtg ccataacat gagcactact ctaccatggt 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccaggacact tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttccttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaaagt 480
tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttc aaagtaaaaa 540
aaaaaaaaa aaaaaaa 557

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<210> 385
<211> 337
<212> DNA
<213> Homo sapiens

<400> 385

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ttcccagggtg atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
ttcacaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300
ctttggccac caattcccc tttccacat cccggca 337

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<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

<400> 386

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gggcccgcga cgggccagg cccgcctcg cgagtcctcc tccccgggtg cctgcccgcga 60
gcccgtcgg cccagagggt gggcgcggg ctgcctctac cggctggcgg ctgtaactca 120
gcgaccttg cccgaaggct ctagcaagga cccaccgacc ccagccggcg cggcgcgggc 180
gcggactttg cccggtgtgt gggcgggagc ggactgcgtg tccgcggacg ggcagcgaag 240
atgttagcct tcgtgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

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<210> 387
<211> 537
<212> DNA
<213> Homo sapiens

<400> 387

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gggccgagtc gggcaccaag ggactctttg caggcttcct tcctcggatc atcaaggctg 60
ccccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg ggcggtgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttctc agcactgagg 240
gagggggcct gtttcccttc cctcccggcg acaagctcca gggcagggct gtccctctgg 300
gcgggccagc acttcctcag acacaacttc ttctgctgc tccagtcgtg gggatcatca 360
cttaccacc cccaagttc aagaccaa atccagctg ccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctgagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaa aaaaaa 537

```

<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

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aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgagggttaaa ccagtttgca ttccccta atgtgaaaaag taagaggact actcagcact 120
gtttgaagat tgccctctct acagcttctg agaattgtgt tatttcactt gccaaagtga 180
ggacccctc cccaacatgc ccagccccc ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgtg gacctacca gagaccagga gggtttggtt agctcacagg 300
acttcccca cccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360
tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctggttatta taaacagaaa 420
atctttcctc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttaa tgggtgggtt ttttcttgtt 520

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<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

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gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgacttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctacccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctg ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

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<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

```

tgccctccca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacgntt ctcatgggtg tggaacatct ctgcttgagg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

```

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(325)
 <223> n = A,T,C or G

<400> 391
 tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncca tgcangcttt 60
 ctctcgccg cagcctggag ctgctcctgg catctacca caatcagncg aggcgagcag 120
 tagccagggc actgctgcc aacagccagtc cnnataccat catgtnaccc ggtgngctct 180
 naantngat ntccanagcc ctacccatcn tagttctgct ctcccacgg ntaccagccc 240
 cactgccag gaatcctaca gccagtacc tgtcccgacg tctctaccta ccagtacgat 300
 gagacctccg gctactacta tgacc 325

<210> 392
 <211> 277
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(277)
 <223> n = A,T,C or G

<400> 392
 atattgttta actccttcct ttatatcttt taacattttc atggngaaa gttcacatct 60
 agtctcactt nggcnagnn ctctacttg agtctcttcc ccggcctggn ccagtnghaa 120
 antaccanga accgncatgn cttaanaacn ncctgggttn tgggttnntc aatgactgca 180
 tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
 ctgaggatag agcgccgcgt cctgtgttgc tggggaa 277

<210> 393
 <211> 566
 <212> DNA
 <213> Homo sapiens

<400> 393
 actagtcag tgtggtggaa ttccgcccgc cgtcgacgga caggtcagct gtctggctca 60
 gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacggt 120
 ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
 gagaaggctc agtttgtcca tcagcattat catgatata ggactgggta cttgggtaag 240
 gaggggtcta ggagatctgt cctttttaga gacaccttac ttataatgaa gtatttggga 300
 ggggtgtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
 catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
 ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
 cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
 ttttgcttat caaaaaaaaa aaaaaa 566

<210> 394
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(384)
 <223> n = A,T,C or G

<400> 394
 gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
 tgcaaatng gaccgggcca aggcctggact gctggagcgt gtgaaggagc tacaggccna 120
 gcaggaggac cgggctttaa ggagttttaa gctgagtgct actgtagacc ccaaatacca 180
 tcccaagatt atcgggagaa agggggcagc aattacccaa atccggttgg agcatgacgt 240

```

gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384

```

```

<210> 395
<211> 399
<212> DNA
<213> Homo sapiens

```

```

<400> 395
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggg 360
gcagcctggt gagaccatcc aatcccaaata aaaatgcac 399

```

```

<210> 396
<211> 403
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

```

```

<400> 396
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata tttttctctaa aaagattcct tgaaacacat 240
taggaaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gttttagggga gggagtgagg gataaaaaga ggaaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403

```

```

<210> 397
<211> 100
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(100)
<223> n = A,T,C or G

```

```

<400> 397
actagtnacg tgtggtggaa ttcgcggccg cgtcgaccta naanccatct ctatagcaaa 60
tccatccccg ctcttggttg gtnacagaat gactgacaaa 100

```

```

<210> 398
<211> 278
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

```

```

<400> 398

```

```

gcgggcgcgt cgacagcagt tccgccagcg ctgcccctg ggtggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

```

```

<210> 399
<211> 298
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

```

```

<400> 399
acggaggtgg aggaagcgn cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
gggggtgccng catggagcgc atgggcgcgg gcctgggcca cgcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggtcatgg accgcatggg ctccgtggag cgcgtgggct 180
ccggcattga gcgcatgggc ccgctgggccc tggaccacat ggctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298

```

```

<210> 400
<211> 548
<212> DNA
<213> Homo sapiens

```

```

<400> 400
acatcaacta cttcctcatt ttaaggatg gcagttccct tcatccctt ttcctgcctt 60
gtacatgtac atgtatgaaa ttctcttctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cacgcttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta ttccatacag gctttgaggc caccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttgccccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctctacc atgggcccc ctctgggat caagccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt 548

```

```

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

```

```

<400> 401
actgtttcca tgttatgttt ctacacattg ctacctcagt gtccttgaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtgcc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
cccttttgca ttgccaagtg ccataacat gagcactact ctaccatggn tctgc 355

```

```

<210> 402
<211> 407
<212> DNA
<213> Homo sapiens

```

<220>
 <221> misc_feature
 <222> (1)...(407)
 <223> n = A,T,C or G

<400> 402
 atggggcgaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
 tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
 aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
 gaataaagat aaaaaagaga aggacattac aaaggtgggc ctgacctttg ataaatctca 240
 ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
 ttgtggagct tctcccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
 gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 403
 cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcacccaa 60
 tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
 tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180
 gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
 tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
 gga 303

<210> 404
 <211> 225
 <212> DNA
 <213> Homo sapiens

<400> 404
 aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
 attgttaatg cactcattta cctttacatg gtgaaagtgc tctcttgatc ctacaaacag 120
 acattttcca ctctgttttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180
 ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405
 <211> 334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(334)
 <223> n = A,T,C or G

<400> 405
 gagctgttat actgtgagtt ctactaggaa atcatcaaatt ctgagggttg tctggaggac 60
 ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120
 tcatcccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggg 180
 ttcccatgtc ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtg 240
 ctgggtgcgt tgtgcctcca gcttctgtc agtgcttcac ggacagtgtc cagcccatgt 300
 cactctccac tctctcanng tggatccac ccct 334

<210> 406
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(216)
 <223> n = A,T,C or G

<400> 406
 ttctacacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
 gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
 acnaaacaca aatttntatgt tgcaacccttg tttctacacc tgtgggttat gacaaagaca 180
 actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 407
 gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
 gtaaatgcaa taggattaaa aaataaattt gatatacat ggaaacagac aaaaaatatt 120
 gtacaacatt gcacccagtgc tcagattcta cacctggcca ctgaggaagc aagagttaat 180
 cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
 ggaaaattgt catthgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
 tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
 tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413

<210> 408
 <211> 183
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(183)
 <223> n = A,T,C or G

<400> 408
 ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
 tncettaacta gttaatcctt aaagggtan ntaatcctta actagtcctt ccattgtgag 120
 cattatcctt ccagtattcn ccttctnttt tatttactcc ttcctggcta cccatgtact 180
 ntt 183

<210> 409
 <211> 250
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(250)
 <223> n = A,T,C or G

<400> 409
 cccacgcatg ataagctctt tatttctgta agtcttgcta ggaaatcatc aaatctgacg 60
 gtgggttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
 gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
 gcttccagtg gcccccagga cagcgtgggc tatgtttaca gcgcttcctt gctggggggg 240
 ggcctatgac 250

132

<210> 410
 <211> 306
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(306)
 <223> n = A,T,C or G

<400> 410
 ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
 agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
 cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaga cacatcctaa 180
 aagggtgttg aatggtgaaa accgcttctt tctttattgc cccttcttat ttatgtgaac 240
 nactggttgg ctttttttgn atctttttta aactggaaaag ttcaattgng aaaatgaata 300
 tcntgc 306

<210> 411
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(261)
 <223> n = A,T,C or G

<400> 411
 agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
 ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
 tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
 aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
 cttctctcaa gngaggcaa a 261

<210> 412
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(241)
 <223> n = A,T,C or G

<400> 412
 gttcaatggt acctgacatt tctacaacac cccactcacc gatgtattcg ttgccagtg 60
 ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
 actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
 ctgggagatt tcaactggga cattgaattc ccaaactacc cangcaatta cccagccaac 240
 a 241

<210> 413
 <211> 231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(231)
 <223> n = A,T,C or G

```

<400> 413
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtag cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagttttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gaggggtcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

```

```

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

```

```

<400> 414
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca 234

```

```

<210> 415
<211> 217
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(217)
<223> n = A,T,C or G

```

```

<400> 415
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttotca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217

```

```

<210> 416
<211> 213
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

```

```

<400> 416
atgcatatnt aaagganact gcctcgcttt tagaagacat ctggnetgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggtaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag 213

```

```

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

```

```

<400> 417
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60

```

134

```

gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggacca cagtatanan aaacctttta 300
agt 303

```

```

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

```

```

<400> 418
tttttggcgg tgggtggggca gggacggggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240
tcagnngtca ggctgggtct aaactcctga cctcaagtga tctgccacc tcagcctccc 300
aaagtgtan gattacaggc cgtgagcc 328

```

```

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

```

```

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
accctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttctt ctctgtgggt ccattcatag cacagtgtgt gactgaggc ttgtgcaggc 180
cgagcaaggc caagctgggt caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaata gcacatcagt tcttctaccc 300
taaaggtagg actaaagggc atctgctttt ctgaagtctt ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

```

```

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

```

```

<400> 420
gttctctcta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttgggt tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgacttttgt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg acaaacctgg caagcccg 408

```

```

<210> 421
<211> 352
<212> DNA
<213> Homo sapiens

```

<220>
 <221> misc_feature
 <222> (1)...(352)
 <223> n = A,T,C or G

<400> 421
 gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
 gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
 ttcactgaca gaacagggtct tttttgggtc cttcttctcc accacnatac atttgcaatc 180
 ctccctcttg aagattcttt ggcagttgtc tttgtcataa cccacagggtg tagaaacaag 240
 ggtgcaacat gaaattttctg tttcgtagca agtgcatgtc tcacaagttg gcangtctgc 300
 cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352

<210> 422
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 422
 atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcataatccag cccaagctgg 60
 cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtgggtcaagg 120
 gcgatagcaa ggtgccggcg atcgccggcg cgtcaatcct ggccaagggtc agccgtgatc 180
 gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcgccggg cataagggtc 240
 atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
 gcttcttccg ccggtacggc tggcctatga aaattat 337

<210> 423
 <211> 310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

<400> 423
 gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
 aggagaatga ggcctggcct gggagccctg tgccctacta aagcncatta gattatccat 120
 tcaactgacg aacaggctct ttttgggtcc ttcttctcca ccacgatata cttgcagtc 180
 tccttcttga agattctttg gcagttgtct ttgtcataac ccacagggtg anaacaagg 240
 gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgcc 300
 tccgagttta 310

<210> 424
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(370)
 <223> n = A,T,C or G

<400> 424
 gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
 ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
 cactgacaga acaggctctt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
 ccttcttgaa gattctttgg cagttgtctt tgtcataacc cacagggtga gaaacatcct 240
 ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
 cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
 tccgtcgacg 370

136

<210> 425
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(216)
 <223> n = A,T,C or G

<400> 425
 aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaataga 60
 taacaacnca acatcaagg n aaananaaca ggaatggntg actntgcata aatngggccga 120
 anattatcca tta ntntaag ggttgacttc aggn tacagc acacagacaa acatgcccag 180
 gaggnntntca ggaccgctcg atgtntntng aggagg 216

<210> 426
 <211> 596
 <212> DNA
 <213> Homo sapiens

<400> 426
 cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60
 tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120
 gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180
 gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
 gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaagaggca cttcccgtta 300
 ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
 aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
 ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
 atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
 gtcccgcgtgg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

<210> 427
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(107)
 <223> n = A,T,C or G

<400> 427
 gaagaattca agtttaggttt attcaaagg g cttacngaga atcctanacc caggncccag 60
 cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

<210> 428
 <211> 38
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(38)
 <223> n = A,T,C or G

<400> 428
 gaacttcna anaangactt tattcactat ttacatt

38

<210> 429

137

<211> 544
 <212> DNA
 <213> Homo sapiens

<400> 429
 ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
 attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
 atatccacga actccttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
 tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcggt 240
 gccttccact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300
 agataactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
 tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagccac 420
 gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
 acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggt gtaggagaga 544
 ttat

<210> 430
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 430
 cttatcncaa tggggctccc aaacttggct gtgcagtga aactccgggg gaattttgaa 60
 gaacactgac acccatcttc caccgccgaca ctctgattta attgggctgc agtgagaaca 120
 gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttgtg atctttgccn 180
 ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgagggg gttccaggag 240
 attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
 caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
 tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
 cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaaagt 480
 ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431
 <211> 392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 431
 gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
 aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aacctatc 120
 tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
 aagagatggg aaacaaaatc ccaggagtgt tgtgtgtgga gtcctgggtt ttccaacaga 240
 catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
 acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
 gcaatgagtc tggcttttac tctgctgttt ct 392

<210> 432
 <211> 387
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(387)
 <223> n = A,T,C or G

<400> 432
 ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
 aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
 ngtagtccaa gctctcggna gtccageccac tgnгааacat gctcccttta gattaacctc 180
 gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
 attctgttgc ttctggggca tttccttgng atgcagagga ccaccaçaca gatgacagca 300
 atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtaç aggaccggga 360
 acaacgtata gaacactgga gtccttt 387

<210> 433
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(281)
 <223> n = A,T,C or G

<400> 433
 ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
 ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
 caggcncat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggçgctggag 180
 atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gccactggg 240
 tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434
 <211> 484
 <212> DNA
 <213> Homo sapiens

<400> 434
 ttttaaaata agcatttagt gctcagtcçc tactgagtag tctttctctc ccctcctctg 60
 aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
 tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
 tttttcccca ttggaactag tcattaaccç atctctgaac tggtagaaaa acatctgaag 240
 agctagctta tcagcatctg acagggtgaat tggatggttc tcagaaccat ttcaccaga 300
 cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccç 360
 tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
 tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
 tttta 484

<210> 435
 <211> 424
 <212> DNA
 <213> Homo sapiens

<400> 435
 gçgççgtcga gagcaggtea ctttctgcct tccacgtcct ccttcaagga agccçcatgt 60
 gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccçacca 120
 cgatcgggca agtaaaccçc ctcçctcgcc gacttcggaa ctggcgagag ttcagcgag 180
 atgggçctgt ggggaggggg caagatagat gagggggagc ggcatggtgc ggggtgaccc 240
 cttggagaga ggaaaaaggc cacaagaggg gctgçcaccg cactaacgg agatggçcct 300
 ggtagagacc tttgggggtc tggaaçctct ggactcccca tgctctaact cccacactct 360
 gctatcagaa acttaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
 aaac 424

<210> 436

<211> 667
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(667)
 <223> n = A,T,C or G

<400> 436
 accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
 tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
 agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
 cagttcctga aaggcaggtg tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
 atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
 gccagggttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
 tgttcatgtt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420
 agttcataat gctgctccat gcccagctgg gtgagttggc caaatccttg tggccatgag 480
 gattccttta tggggtcagt gggaaaagggt tcaatgggac ttcgggtctcc atgccgaaac 540
 accaaagtca caaacttcaa ctccttggct agtacacttc ggtctagcca gaaaaaaggc 600
 agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
 tgttgag 667

<210> 437
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 437
 ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
 acacagccag gtaaggaaag ctggattggc aactaggac tctaccatac cgggttttgt 120
 taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
 ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
 aggtactcct ctattttcac cctcttctgt tctactctct ggcagtcaga cctgtgggag 300
 gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
 catttctcca gggtacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
 atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
 acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
 tcctatttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
 taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
 ctgcatcatg tgctctcttg gctgaaaatg acc 693

<210> 438
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 438
 ctgcttatca caatgaatgt tctcctgggc agcgttggtga tctttgccac cttcgtgact 60
 ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
 atgtttctac acctgtgggt tatgacaaa acaactgcc aagaatcttc aagaaggagg 180
 actgcaagta tatctgggtg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
 gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctctctg 300
 gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

<210> 439
 <211> 431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

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gttcctnnta actcctgcc aaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcgcccgcg 420
aatttagtag t                                     431

```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

<400> 440

```

agagataaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaattgtc tgaatggaa cagatttcaa aaaaaaacc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta                                     523

```

<210> 441

<211> 430

<212> DNA

<213> Homo sapiens

<400> 441

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gttcctccta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcgcccgcg 420
aatttagtag                                     430

```

<210> 442

<211> 362

<212> DNA

<213> Homo sapiens

<400> 442

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ctaaggaatt agtagtgttc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcctggaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc                                     362

```

<210> 443

<211> 624

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(624)
 <223> n = A,T,C or G

<400> 443
 tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
 ttgaaagaat taaattcaga ggaggggaga gaaagagtag tcagtaggga ctgagcacta 120
 aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
 tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
 cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
 tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360
 taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtag 420
 atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgcta 480
 agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
 ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
 ttgtccctat ctgctaaaca gatac 624

<210> 444
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(425)
 <223> n = A,T,C or G

<400> 444
 gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
 gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
 ttcattgcta tagcataaca caaaatttgc ataagtgtg gtcagcaaat ccttgaatgc 180
 tgcttaattgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
 gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
 cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
 ggaggcacca gggcataagt gagtagactt atggctgacg cgcccgcgaa ttttagtagta 420
 gtaga 425

<210> 445
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(414)
 <223> n = A,T,C or G

<400> 445
 catgtttatg nttttggatt actttgggca cctagtgttt ctaaaatcgtc tatcattctt 60
 ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
 tgaaattctt tgcatgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
 tgggtgtgtt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
 aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
 ggatttttat aatcctactc acaaatgact aggtctctcc tcttgtattt tgaagcagt 360
 tgggtgctgg attgataaaa aaaaaaaaaa tcgacgcggc cgcaattta gtag 414

<210> 446
 <211> 631
 <212> DNA
 <213> Homo sapiens

142

<220>
 <221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 446
 acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
 tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
 atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
 ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
 ctgtcatctg tgtggtgggc ctctgcatca caagggccaa actttaggta atagcattgg 300
 actgagattt gtaaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
 gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
 taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttggg ctacacaata 480
 cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccttg catttgggtg 540
 aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatattga 600
 aatagtatac attgtcttga tgttttttct g 631

<210> 447
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(585)
 <223> n = A,T,C or G

<400> 447
 ccttgggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60
 cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
 gccctctctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
 agttcctgaa aggcagggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
 tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
 ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
 gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
 gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
 attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
 ccaaagtcac aaacttcaac tccttggtga gtacacttcg gtcta 585

<210> 448
 <211> 93
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(93)
 <223> n = A,T,C or G

<400> 448
 tgctcgtggg tcattctgan nnccgaactg acctgcccag ccctgccgan gggccnccat 60
 ggctccctag tgccctggag agganggggc tag 93

<210> 449
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(706)

<223> n = A,T,C or G

<400> 449

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<210> 450

<211> 493

<212> DNA

<213> Homo sapiens

<400> 450

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gcgaatttag tag 493

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<210> 451

<211> 501

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 451

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cgcncacagc actcacagct actcaggagg ctgagaacac gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggcnctgcn cccagcatg gatgacagag tgaactcca 480
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<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(51)

144

<223> n = A,T,C or G

<400> 452

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<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

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taacaaaccc	tgctccaatc	tgtcacataa	aagtctgtga	cttgaagttt	antcagcacc	240
cccacaaac	tttatttttc	tatgtgtttt	ttgcaacata	tgagtgtttt	gaaaataagg	300
tacccatgtc	tttatta					317

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

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agaagaccaa	attcttctgc	atcccagctt	gcaaacaaaa	ttgttcttct	aggtctccac	180
ccttcctttt	tcagtgttcc	aaagctcctc	acaatttcat	gaacaacagc	t	231

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

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gtttcaacgc	attgatgact	tctccaagga	tcttcctttg	gcacgacca	cattcagggg	180
caaagaattt	ctcatagcac	agctcacaat	acagggtctc	tttctcctct	a	231

<210> 456

<211> 231

<212> DNA

<213> Homo sapiens

<400> 456

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tgactcaaaa	ttcctttatc	aggaataact	acatagccac	tatttaca	gccattggaa	180
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<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

145

<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

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tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458
<211> 231
<212> DNA
<213> Homo sapiens

<400> 458
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acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
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<210> 459
<211> 231
<212> DNA
<213> Homo sapiens

<400> 459
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gccctgcact gttttccctc caccacagcc atctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460
<211> 231
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<213> Homo sapiens

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cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
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<210> 461
<211> 231
<212> DNA
<213> Homo sapiens

<400> 461
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<210> 462
<211> 231
<212> DNA
<213> Homo sapiens

<400> 462
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tctagaggag gtattttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463
<211> 231
<212> DNA
<213> Homo sapiens

<400> 463
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tggggagggtg gatcttccag tcgaagcggc atagaagccc gtgtgaaaag c 231

<210> 464
<211> 231
<212> DNA
<213> Homo sapiens

<400> 464
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cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
ggtgccagcg caccagctag atgctctgta acttctagcc cccattttcc c 231

<210> 465
<211> 231
<212> DNA
<213> Homo sapiens

<400> 465
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aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
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<210> 466
<211> 231
<212> DNA
<213> Homo sapiens

<400> 466
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cctgtgcaat caaatattgt ggagaattcc ctactggag aagtcacaaa gactatagga 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgaggct g 231

<210> 467
<211> 311
<212> DNA
<213> Homo sapiens

<400> 467
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<210> 468
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147

<212> DNA

<213> Homo sapiens

<400> 468

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<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

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<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

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agaaagggtca cagtacagat ctgggaacta aatattaaaa atgagtgtgg ctggatatat 1140
ggagaatgtt gggcccagaa ggaaccgtag agatcagata ttacaacagc tttgttttga 1200
gggttagaaa tatgaaatga tttggttatg aacgcacagt ttaggcagca gggccagaat 1260
cctgaccctc tgccccgtgg ttatctctc cccagcttgg ctgcctcatg tcatcacagt 1320
attccatttt gtttgttgca tgtcttgtga agccatcaag attttctcgt ctgttttctt 1380
ctcattggta atgctcactt tgtgacttca tttcaaactc gtaatcccgt tcaaataaat 1440
atccacaaca ggatctgttt tcctgcccat cctttaagga acacatcaat tcattttcta 1500
atgtccttcc ctcacaagcg ggaccaggca cagggcgagg ctcatcgatg acccaagatg 1560
gcggccgggc atttctccca gggatctctg tgcttccttt tgtgcttcct gtgtgtgtgg 1620
atatttaaag gggctggaaa tgtgcaaaaa catgtcacta cttagacatt atattgtcat 1680
cttgcgtgtt ctagtgtgt taattatctc catttcagca gatgtgtggc ctcataggtg 1740
aaagtacaga gcctttctta tttctcactt ggaaatacat acgaccattt gaggagacaa 1800
atggcaaggt gtcagcatac cctgaacttg agttgagagc tacacacaat attattggtt 1860
tccgagcatc acaaacaccc tctctgtttc ttcactgggc acagaatttt aatacttatt 1920
tcagtgggct gttggcagga acaaatgaag caatctacat aaagtcacta gtgcagtggc 1980
tgacacacac cattctcttg aggtccctc tagagatccc acaggtcata tgacttcttg 2040
gggagcagtg gctcacacct gtaatcccag cactttggga ggctgaggca ggtgggtcac 2100
ctgaggctcag gagttcaaga ccagcctggc caatatggtg aaaccccatc tctactaaaa 2160
atacaaaaat tagctgggcg tgctggtgca tgctgtaat cccagctact tgggaggctg 2220
aggcaggaga attgctggaa catgggaggc ggaggttgca gtgagctgta attgtgccat 2280
tgactctgaa cctgggagac agagtgggaa tctgtttcca aaaaacaaac aaacaaaaaa 2340
ggcatagtca gatacaacgt ggggtgggatg tgtaaataga agcaggatat aaagggcatg 2400
gggtgacggg tttgccaac acaatg

```

```

<210> 471
<211> 812
<212> DNA
<213> Homo sapiens

```

```

<400> 471
gaacaaaatg agtaatgtta ttctacagtg tagaaaaggtc acagtacaga tctgggaact 60
aatattaaaa aatgagtgtg gctggatata tggagaatgt tgggcccaga aggaaccgta 120
gagatcagat attacaacag ctttgttttg agggtttaga atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcctgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcatcacag tattecattt tgtttgttgc atgtcttgtg 300
aagccatcaa gattttctcg tctgttttcc tctcattggt aatgctcact ttgtgacttc 360
atttcaaatac tgtaatcccg ttcaaataaa tatccacaac aggatctgtt ttctgccca 420
tcctttaagg aacacatcaa ttcattttct aatgtccttc cctcacaagc gggaccaggc 480
acagggcgag gctcatcgat gaccacaagat ggcgccggg catttctccc agggatctct 540
gtgtctcctt ttgtgcttcc tgtgtgtgtg gatattttaa ggggctggaa atgtgcaaaa 600
acatgtcact acttagacat tatattgtca tcttgctgtt tctagtgtat ttaattatct 660
ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agccttctt atttctcacc 720
tctgtatcat caggtccttc ccaccatgca gatcttctcg gtctccctcg gctgcagcca 780
cacaaatctc ccctctgttt ttctgatgcc ag
812

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<210> 472
<211> 515
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(515)
<223> n = A,T,C or G

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<400> 472
acgggagactt attttctgat attgtctgca tatgtatgtt ttttaagagtc tggaaatagt 60
cttatgactt tcctatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120
gttccagaat tattggctct tgacagcccg tgaatctcag caagaggaac caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240

```

150

```

agtagaaggt gattgccagg aaatggatct ggaaaagact cggagtggagc gtggagatgg 300
ctctgatgta aaagagaaga ctccaccta tccctaagcat gctaagacta aagaagcagg 360
agatgggcag ccataagtta aaaagaagac aagctgaagc tacacacatg gctgatgtca 420
cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaa aaanaaaan aaaaaa 515

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<210> 473
 <211> 750
 <212> PRT
 <213> Homo sapiens

<400> 473
 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
 5 10 15
 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
 20 25 30
 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
 35 40 45
 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
 50 55 60
 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
 65 70 75 80
 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
 85 90 95
 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
 100 105 110
 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
 115 120 125
 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
 130 135 140
 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
 145 150 155 160
 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
 165 170 175
 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
 180 185 190
 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
 195 200 205
 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
 210 215 220
 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
 225 230 235 240
 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
 245 250 255
 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr

260										265										270									
Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly														
		275						280				285																	
Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys														
		290				295					300																		
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg														
305					310					315					320														
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn														
				325					330					335															
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val														
			340					345					350																
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro														
		355					360					365																	
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly														
		370				375					380																		
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg														
385					390					395					400														
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile														
				405					410					415															
Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr														
			420					425					430																
Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala														
		435					440					445																	
Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val														
	450					455					460																		
Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu														
465					470					475					480														
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser														
				485					490					495															
Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile														
			500					505					510																
Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu														
		515					520				525																		
Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn														
		530				535					540																		
Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr	Tyr	Glu														
545					550				555						560														
Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val														
				565					570					575															
Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val														
			580					585					590																

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 595 600 605
 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
 610 615 620
 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
 625 630 635 640
 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
 645 650 655
 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
 660 665 670
 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 675 680 685
 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
 690 695 700
 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
 705 710 715 720
 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
 725 730 735
 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 740 745 750

<210> 474
 <211> 386
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 5 10 15
 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 20 25 30
 Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
 35 40 45
 Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
 50 55 60
 Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
 65 70 75 80
 Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
 85 90 95
 Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
 100 105 110
 Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
 115 120 125
 Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His

153

130 135 140
 Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
 145 150 155 160
 Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
 165 170 175
 Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
 180 185 190
 Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
 195 200 205
 Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro
 210 215 220
 Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu
 225 230 235 240
 Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser
 245 250 255
 Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys
 260 265 270
 Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala
 275 280 285
 His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn
 290 295 300
 Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe
 305 310 315 320
 Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln
 325 330 335
 His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro
 340 345 350
 Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp
 355 360 365
 Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly Thr Glu Asp Ser
 370 375 380
 Thr Asp
 385

<210> 475
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
 5 10 15
 Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
 20 25 30

155

Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His Pro
 50 55 60
 Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val Ile
 65 70 75 80
 Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln Val
 85 90 95
 Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser Leu
 100 105 110
 Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp Leu
 115 120 125
 Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val Lys
 130 135 140
 Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr
 145 150 155 160
 Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Thr Pro Lys
 165 170 175
 Lys Leu Gln Cys Val Asp Leu His Val Ile Ser Asn Asp Val Cys Ala
 180 185 190
 Gln Val His Pro Gln Lys Val Thr Lys Phe Met Leu Cys Ala Gly Arg
 195 200 205
 Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp Ser Gly Gly Pro Leu
 210 215 220
 Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser Trp Gly Ser Glu Pro
 225 230 235 240
 Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val Val His Tyr
 245 250 255
 Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Gly Ser Met Ala
 260 265 270
 Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile Leu Gly
 275 280 285
 Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly
 290 295 300
 Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 305 310 315 320
 Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
 325 330 335
 Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
 340 345 350
 Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
 355 360 365
 Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
 370 375 380

Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
 385 390 395 400
 Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
 405 410 415
 Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
 420 425 430
 Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
 435 440 445
 Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
 450 455 460
 Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
 465 470 475 480
 Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
 485 490 495
 Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
 500 505 510
 Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser Glu Phe Met Val
 515 520 525
 Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu
 530 535 540
 Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala Ala
 545 550 555 560
 Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu
 565 570 575
 Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val
 580 585 590
 Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr
 595 600 605
 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu
 610 615 620
 Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys
 625 630 635 640
 Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly
 645 650 655
 Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu
 660 665 670
 Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser
 675 680 685
 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu
 690 695 700
 Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr

705	710	715	720
Gln Glu Glu Cys	Leu Phe Gly Leu Leu Thr	Leu Ile Phe Leu Thr Cys	
	725	730	735
Val Ala Ala Thr	Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr		
	740	745	750
Glu Pro Ala Glu Gly Leu Ser	Ala Pro Ser Leu Ser Pro His Cys Cys		
	755	760	765
Pro Cys Arg Ala Arg Leu	Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro		
	770	775	780
Arg Leu His Gln Leu Cys Cys Arg Met	Pro Arg Thr Leu Arg Arg Leu		
	785	790	795
Phe Val Ala Glu Leu Cys Ser Trp Met	Ala Leu Met Thr Phe Thr Leu		
	805	810	815
Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg			
	820	825	830
Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg			
	835	840	845
Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe			
	850	855	860
Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val			
	865	870	875
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys			
	885	890	895
Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly			
	900	905	910
Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu			
	915	920	925
Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr			
	930	935	940
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly			
	945	950	955
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly			
	965	970	975
Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys			
	980	985	990
Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val			
	995	1000	1005
Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala			
	1010	1015	1020
Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val			
	1025	1030	1035
			1040

158

Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu
1045 1050 1055

Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser
1060 1065 1070

Asp Leu Ala Lys Tyr Ser Ala
1075